

**Remarks**

In view of the above amendments and the following remarks, reconsideration of the outstanding office action is respectfully requested.

Claim 1 has been amended, claims 3-5 have been cancelled without prejudice, and new claims 10-21 have been added. Descriptive support for new claims 10 and 11 appears in the first full paragraph on page 30 and the third full paragraph on page 35, respectively; descriptive support for new claims 12-14 appears in the first full paragraph on page 34; and descriptive support for new claims 15 and 16 appears in the first full paragraph on page 30. New claim 17 finds descriptive support in original claim 3 (i.e., claim written in independent form), and new claims 18-21 find descriptive support in original claims 4 and 6-8, respectively. Claims 1, 2, and 6-21 are pending.

The objection to the specification is overcome by the above amendments. Although applicants disagree with the assertion made by the U.S. Patent and Trademark (“PTO”), the present claim language is clearly supported by the first full paragraph on page 30, along with the disclosure of the nucleic acid sequence of SEQ ID NO: 177 and the corresponding amino acid sequence of SEQ ID NO: 178.

The objections to claims 1 and 5 are overcome by the above amendments and should be withdrawn.

The rejection of claims 1-9 under 35 U.S.C. §112 (first paragraph) as lacking written descriptive support is respectfully traversed.

The burden of establishing that an application lacks adequate written descriptive support falls on the PTO. *See In re Wertheim*, 541 F.2d 257, 263, 191 USPQ 90, 97 (CCPA 1976) (“[T]he PTO has the initial burden of presenting evidence or reasons why persons skilled in the art would not recognize in the disclosure a description of the invention defined by the claims.”). Hence, the PTO must demonstrate *why* the disclosure is insufficient.

The Federal Circuit has clearly espoused that *per se* conclusions of written description violations cannot be founded upon the basis of genus size alone. *See Enzo Biochem, Inc. v. Gen-Probe Inc.*, 296 F.3d 1316, 1326-27, 63 USPQ2d 1609, 1614-15 (Fed. Cir. 2002) (refusing to adopt position that three species as a matter of law cannot satisfy written description requirement for significantly larger genus). Thus, the PTO’s conclusion

cannot be based on genus size alone. But that is precisely what the PTO has done at pages 3-4 of the outstanding office action. Because the PTO's position is unsupported by law and unsupported by any facts other than genus size, applicants submit that the PTO's position cannot be sustained.

In contrast, applicants present Exhibits 1-3 (attached hereto) as evidence that the nucleic acid sequence of SEQ ID NO: 177 and the corresponding amino acid sequence of SEQ ID NO: 178 represent the claimed genus. Exhibit 1 is a presentation of Genbank accessions for *Bacillus* or *Geobacillus* (formerly *Bacillus*) *holA* nucleic acids that are homologous to the nucleotide sequence of SEQ ID NO: 177. These *holA* nucleic acids were identified by a protein-protein BLAST search of the Genbank database performed using the amino acid sequence of SEQ ID NO: 178 and the BLAST default settings. Homologous sequences were identified in *Geobacillus kaustophilus*, *Bacillus cereus*, *Bacillus anthracis*, *Bacillus thuringiensis*, *Bacillus weihenstephanensis*, *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus halodurans*, and *Bacillus clausii* (Exhibit 1). Based upon alignments performed using Align<sup>®</sup> for nucleic acids and ClustalW for amino acids (using the European Molecular Biology Laboratory server and its default settings), these homologs share between about 51 and about 98 percent identity at the nucleic acid level (Exhibit 2) and between about 37 and about 99 percent identity at the amino acid level (Exhibit 3). Thus, species of delta subunits from organisms that belong to the biological classification *Bacillus* or *Geobacillus* clearly share similar structure and, therefore, function.

Applicants submit that the language recited in claims 1 and 9 is precisely the type of claim language that was acknowledged in *Univ. of California v. Eli Lilly*, 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) as being acceptable under the written description requirement. In *Eli Lilly*, the Federal Circuit addressed the validity of several claims of U.S. Patent No. 4,652,525 to Rutter et al. ("Rutter"), specifically those claims that recited the limitations 'vertebrate,' 'mammalian,' or 'human' cDNA for insulin. Rutter disclosed the nucleotide and amino acid sequences of a rat cDNA encoding insulin, but merely described a general procedure for obtaining the human cDNA encoding insulin. *Id.* at 1567, 43 USPQ2d at 1405. The Federal Circuit found that the description of the rat cDNA did not provide adequate descriptive support for the narrow subgenus of 'human' cDNA (no species disclosed), the larger subgenus of 'mammalian' cDNA (only the one rat species disclosed), and the larger genus of 'vertebrate' cDNA (only the one rat species disclosed). *Id.* at 1567-68, 43 USPQ2d at 1405. The Federal Circuit did acknowledge, however, the district court's

statement that the specification provided adequate written descriptive support for the subgenus of ‘rat’ cDNA encoding insulin. *Id.* at 1566.

Thus, functional language should be acceptable when the genus as claimed is sufficiently limited in scope (i.e., from *Bacillus* or *Bacillus stearothermophilus*) and the specification describes one or more species within that genus. Claims 1 and 9 recite the same type of functional claim language that was identified as acceptable in *Eli Lilly* given the description of a single species by its nucleotide sequence. Thus, it should be evident that claims 1 and 9 (and claims dependent thereon) find written descriptive support in the present application.

It should be noted that the “Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112 ¶ 1, ‘Written Description’ Requirement,” make explicitly clear that the description of a representative number of species does *not* require the description to be of such a nature that it would provide support for each species that the genus embraces. 66 Fed. Reg. 1099, 1106 (2001). Hence, the absence of sequences (in the present specification) for the later-identified *hola* and delta homologs is irrelevant to the issue of whether the present specification provides adequate written descriptive support for their use in accordance with the present invention.

Moreover, the conclusion by the PTO is contrary to evidence submitted herewith by applicants. As demonstrated by Exhibits 1-3, one of ordinary skill in the art would have understood that applicants were in possession of the presently claimed invention at the time the present application was filed. This is so, because persons of skill in the art would have expected sufficiently related organisms from the genus *Bacillus* (and now *Geobacillus*) to possess homologous *hola* nucleotide sequences or delta subunit proteins. Exhibits 1-3 confirm this expectation to have been reasonable.

In view of all of the foregoing, applicants submit that the rejection of claims 1-9 is improper and should be withdrawn.

The rejection of claims 1-9 under 35 U.S.C. §112 (first paragraph) for lack of enablement is respectfully traversed.

It is the position of the PTO that the specification does not provide sufficient guidance for making and using other delta subunit-encoding DNA molecules within the scope of the claims. Applicants respectfully disagree.

The PTO is respectfully reminded that all that is needed is objective enablement of what is claimed. *In re Wright*, 999 F.2d 1557, 1561, 27 USPQ2d 1510, 1513 (Fed. Cir. 1993). The present application provides the nucleotide sequence of *Bacillus* (now

*Geobacillus) stearothermophilus hola* (e.g., SEQ ID NO: 177) and describes how one of ordinary skill can isolate homologs of the disclosed sequence (*see* page 41, line 9 to page 42, line 29), express the delta subunit encoded by such homologous *hola* sequences (*see* Example 19, expressing *A. aeolicus* delta subunit), and test the encoded delta subunit for clamp loader assembly competence (*see* Examples 24 and 25, testing *A. aeolicus* clamp loader assembly) and for clamp loader activity (*see* Examples 26 and 30, testing *A. aeolicus* clamp loader activity). Thus, one of ordinary skill in the art would have been fully able to make and use DNA molecules and their encoded proteins within the scope of the presently claimed invention.

Moreover, with regard to method 3 for homolog identification, described at page 42, that is precisely the approach used to identify the *hola* homologs shown in Exhibit 1 (i.e., from other *Bacillus* or *Geobacillus* organisms). For this reason, it should be apparent that the present application fully enables the production and use of other species of *Bacillus* or *Bacillus* (now *Geobacillus*) *stearothermophilus hola* homologs.

In view of all of the foregoing, applicants submit that the rejection of claims 1-9 for lack of enablement is improper and should be withdrawn.

Because 1 is allowable for the reasons noted above, applicants further submit that new claims 10-16 also are allowable. Consistent with the PTO acknowledgments at pages 3-4 the outstanding office action, applicants further submit that that the specification provides written descriptive support for and enables the claimed DNA molecules that encode the delta subunit including the amino acid sequence of SEQ ID NO: 178 (i.e., claims 17-21).

In view of all of the foregoing, applicant submits that this case is in condition for allowance and such allowance is earnestly solicited.

Respectfully submitted,

Date: August 24, 2006

/Edwin V. Merkel/

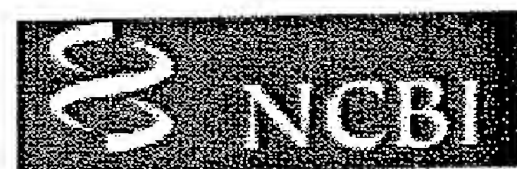
Edwin V. Merkel

Registration No. 40,087

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Rochester, New York 14603-1051  
Telephone: (585) 263-1128  
Facsimile: (585) 263-1600

## **Exhibit 1**





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Show whole sequence

☐ Reverse complemented strand Fer1: BA000043. Reports *Geobacillus kaust...*[gi:56378377]

Links

Features Sequence

LOCUS BA000043 1047 bp DNA linear BCT 04-DEC-2004

DEFINITION *Geobacillus kaustophilus* HTA426 DNA, complete genome.

ACCESSION BA000043 REGION: 2532557..2533603

VERSION BA000043.1 GI:56378377

KEYWORDS

SOURCE *Geobacillus kaustophilus* HTA426

ORGANISM *Geobacillus kaustophilus* HTA426  
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Geobacillus*.

REFERENCE 1

AUTHORS Takami,H., Takaki,Y., Chee,G.J., Nishi,S., Shimamura,S., Suzuki,H., Matsui,S. and Uchiyama,I.

TITLE Thermoadaptation trait revealed by the genome sequence of thermophilic *Geobacillus kaustophilus*

JOURNAL (er) Nucleic Acids Res. 32 (21), 6292-6303 (2004)

PUBMED 15576355

REFERENCE 2 (bases 1 to 1047)

AUTHORS Takami,H., Takaki,Y. and Chee,G.

TITLE Direct Submission

JOURNAL Submitted (25-JUN-2003) Hideto Takami, Japan Marine Science and Technology Center, Microbial Genome Analysis Research Group; 2-15 Natsushima-cho, Yokosuka, Kanagawa 237-0061, Japan  
(E-mail:takamih@jamstec.go.jp,  
URL:http://www.jamstec.go.jp/jamstec-e/bio/exbase.html,  
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ORIGIN

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 ORGANISM *Bacillus* sp. NRRL B-14911  
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
 REFERENCE 1 (bases 1 to 1041)  
 AUTHORS Siefert, J., Ferriera, S., Johnson, J., Kravitz, S., Halpern, A.,  
 Remington, K., Beeson, K., Tran, B., Rogers, Y.-H., Friedman, R. and  
 Venter, J.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-FEB-2006) J Craig Venter Institute, 9704 Medical  
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☐ 1: NZ\_AALL01000072. Reports *Bacillus cereus* s...[gi:89203481]

Links

Comment Features Sequence

LOCUS NZ\_AALL01000072 1011 bp DNA linear BCT 06-MAR-2006

DEFINITION *Bacillus cereus* subsp. cytotoxis NVH 391-98 ctg92, whole genome shotgun sequence.

ACCESSION NZ\_AALL01000072 REGION: complement(4223..5233)

VERSION NZ\_AALL01000072.1 GI:89203481

KEYWORDS WGS.

SOURCE *Bacillus cereus* subsp. cytotoxis NVH 391-98

ORGANISM *Bacillus cereus* subsp. cytotoxis NVH 391-98  
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1011)

AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K., Detter,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E., Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S., Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J., Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S., Nguen-the,C. and Sorokin,A.

CONSRM US DOE Joint Genome Institute (JGI-PGF)

TITLE Sequencing of the draft genome and assembly of *Bacillus cereus* subsp. cytotoxis NVH 391-98

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1011)

AUTHORS Larimer,F. and Land,M.

CONSRM US DOE Joint Genome Institute (JGI-ORNL)

TITLE Annotation of the draft genome assembly of *Bacillus cereus* subsp. NVH 391-98

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1011)

AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K., Detter,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E., Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S., Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J., Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S., Nguen-the,C. and Sorokin,A.

CONSRM US DOE Joint Genome Institute (JGI-PGF)

TITLE Direct Submission

JOURNAL Submitted (02-MAR-2006) US DOE Joint Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

COMMENT URL -- <http://www.jgi.doe.gov>  
Contact: Paul Richardson (microbes@cuba.jgi-psf.org)  
Draft sequencing done at US DOE Joint Genome Institute  
Source DNA and bacteria available from Alexei Sorokin (alexei.sorokine@jouy.inra.fr)  
The JGI and collaborators endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to follow them. It is our intention to publish the work of this

project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>)

#### Notes:

*Bacillus cereus* NVH 398-91 was originally isolated as a contaminant of vegetable puree in a retirement house in Essone (France) by Marie-Laure De Buyser (AFSSA, France). The strain was identified as a cause of a severe food poisoning case. It was further characterized biochemically and a novel cytotoxin K was identified as a major cause of epithelial cell lysis leading to necrotic enteritis (Lund et al, Mol Microbiol, 2000, 38, 254). Although the strain was identified as *Bacillus cereus*, it appeared to be different from all known strains. Detailed phylogenetic studies using MLST approach placed the strain rather far from main strain clusters, but confirmed that the strain belongs to the *B. cereus* group (Sorokin et al, Appl Env Microbiol, 2006, 72, 1569). Genomic sequence clearly indicated that the strain is very different from other representatives of the group and should be assigned a new species status, for which we propose a name *Bacillus cytotoxis*. However, assigning of the novel species status is hampered by the fact that only one such strain is described at the moment of genomic sequencing being done (2005).

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Range: from 4137069 to 4138079

Show whole sequence

☐ Reverse complemented strand Fe☐ 1: AE017334. Reports *Bacillus anthracis*...[gi:50082967]

Links

Comment Features Sequence

LOCUS AE017334 1011 bp DNA linear BCT 09-JUL-2004

DEFINITION *Bacillus anthracis* str. 'Ames Ancestor', complete genome.

ACCESSION AE017334 REGION: 4137069..4138079

VERSION AE017334.2 GI:50082967

KEYWORDS

SOURCE *Bacillus anthracis* str. 'Ames Ancestor'

ORGANISM *Bacillus anthracis* str. 'Ames Ancestor'

Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1011)

AUTHORS Ravel,J., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z., Federova,N.B., Wilson,M., Stanley,S., Decker,S., Read,T.D., Salzberg,S. and Fraser,C.M.

TITLE *Bacillus anthracis* comparative genomics

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1011)

AUTHORS Ravel,J., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z., Federova,N.B., Salzberg,S. and Fraser,C.M.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

REFERENCE 3 (bases 1 to 1011)

AUTHORS Ravel,J., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z., Federova,N.B., Salzberg,S. and Fraser,C.M.

TITLE Direct Submission

JOURNAL Submitted (09-JUL-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

REMARK Sequence update by submitter

COMMENT On Jul 9, 2004 this sequence version replaced gi:47500402.

FEATURES

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gene complement(1..1011)

/locus\_tag="GBAA4548"

CDS complement(1..1011)

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## ORIGIN

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Range: from 4085571 to 4086581

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☐ Reverse complemented strand Fea☐ 1: NC\_003909. Reports *Bacillus cereus* A...[gi:42779081]

Links

Comment Features Sequence

LOCUS NC\_003909 1011 bp DNA linear BCT 17-JAN-2006

DEFINITION *Bacillus cereus* ATCC 10987, complete genome.

ACCESSION NC\_003909 REGION: 4085571..4086581

VERSION NC\_003909.8 GI:42779081

PROJECT GenomeProject:74

KEYWORDS .

SOURCE *Bacillus cereus* ATCC 10987

ORGANISM *Bacillus cereus* ATCC 10987  
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1011)

AUTHORS Rasko,D.A., Ravel,J., Okstad,O.A., Helgason,E., Cer,R.Z., Jiang,L., Shores,K.A., Fouts,D.E., Tourasse,N.J., Angiuoli,S.V., Kolonay,J., Nelson,W.C., Kolsto,A.-B., Fraser,C.M. and Read,T.D.

TITLE The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic adaptations and a large plasmid related to *Bacillus anthracis* pX01

JOURNAL Nucleic Acids Res. 32 (3), 977-988 (2004)

PUBMED 14960714

REFERENCE 2 (bases 1 to 1011)

CONSRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (10-SEP-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 1011)

AUTHORS Rasko,D.A., Ravel,J., Okstad,O.A., Helgason,E., Cer,R.Z., Jiang,L., Shores,K.A., Fouts,D.E., Tourasse,N.J., Angiuoli,S.V., Kolonay,J., Nelson,W.C., Kolsto,A.-B., Fraser,C.M. and Read,T.D.

TITLE Direct Submission

JOURNAL Submitted (19-FEB-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from AE017194. On Feb 24, 2004 this sequence version replaced gi:29653128. COMPLETENESS: full length.

FEATURES

source Location/Qualifiers

1..1011

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CDS complement(1..1011)

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## ORIGIN

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☐ 1: [NZ\\_AAJM01000393](#). Reports *Bacillus thuringi...*[gi:75763390]

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[Features](#) [Sequence](#)

LOCUS NZ\_AAJM01000393 1011 bp DNA linear BCT 16-SEP-2005

DEFINITION *Bacillus thuringiensis* serovar israelensis ATCC 35646 sq1546, whole genome shotgun sequence.

ACCESSION [NZ\\_AAJM01000393](#) REGION: complement(97..1107)

VERSION [NZ\\_AAJM01000393.1](#) GI:75763390

KEYWORDS WGS.

SOURCE *Bacillus thuringiensis* serovar israelensis ATCC 35646

ORGANISM *Bacillus thuringiensis* serovar israelensis ATCC 35646  
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1011)

AUTHORS Anderson, I., Sorokin, A., Kapatral, V., Reznik, G., Bhattacharya, A., Mikhailova, N., Burd, H., Joukov, V., Kaznadzey, D., Walunas, T., D'Souza, M., Larsen, N., Pusch, G., Liolios, K., Grechkin, Y., Lapidus, A., Goltsman, E., Chu, L., Fonstein, M., Ehrlich, D., Overbeek, R., Kyrpides, N. and Ivanova, N.

TITLE Comparative genome analysis of *Bacillus cereus* group genomes with *Bacillus subtilis*

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1011)

AUTHORS Anderson, I., Sorokin, A., Kapatral, V., Reznik, G., Bhattacharya, A., Mikhailova, N., Burd, H., Joukov, V., Kaznadzey, D., Walunas, T., D'Souza, M., Larsen, N., Pusch, G., Liolios, K., Grechkin, Y., Lapidus, A., Goltsman, E., Chu, L., Fonstein, M., Ehrlich, D., Overbeek, R., Kyrpides, N. and Ivanova, N.

TITLE Comparative genome analysis of *Bacillus cereus* group genomes with *Bacillus subtilis*

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1011)

AUTHORS Anderson, I., Sorokin, A., Kapatral, V., Reznik, G., Bhattacharya, A., Mikhailova, N., Burd, H., Joukov, V., Kaznadzey, D., Walunas, T., D'Souza, M., Larsen, N., Pusch, G., Liolios, K., Grechkin, Y., Lapidus, A., Goltsman, E., Chu, L., Fonstein, M., Ehrlich, D., Overbeek, R., Kyrpides, N. and Ivanova, N.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-2005) Integrated Genomics, Inc., 2201 West Campbell Park Dr, Chicago, IL 60612, USA

REFERENCE 4 (bases 1 to 1011)

AUTHORS Anderson, I., Sorokin, A., Kapatral, V., Reznik, G., Bhattacharya, A., Mikhailova, N., Burd, H., Joukov, V., Kaznadzey, D., Walunas, T., D'Souza, M., Larsen, N., Pusch, G., Liolios, K., Grechkin, Y., Lapidus, A., Goltsman, E., Chu, L., Fonstein, M., Ehrlich, D., Overbeek, R., Kyrpides, N. and Ivanova, N.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-2005) Integrated Genomics, Inc., 2201 West Campbell Park Dr, Chicago, IL 60612, USA

FEATURES Location/Qualifiers

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## ORIGIN

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☐ 1: [NZ\\_AAOY01000019](#). Reports *Bacillus weihenst...*[gi:89206281]

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LOCUS NZ\_AAOY01000019 1011 bp DNA linear BCT 06-MAR-2006

DEFINITION *Bacillus weihenstephanensis* KBAB4 ctg244, whole genome shotgun sequence.

ACCESSION [NZ\\_AAOY01000019](#) REGION: complement(8181..9191)

VERSION [NZ\\_AAOY01000019.1](#) GI:89206281

KEYWORDS WGS.

SOURCE *Bacillus weihenstephanensis* KBAB4

ORGANISM *Bacillus weihenstephanensis* KBAB4  
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1011)

AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K., Detter,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E., Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S., Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J., Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S., Nguen-the,C. and Sorokin,A.

CONSRTM US DOE Joint Genome Institute (JGI-PGF)

TITLE Sequencing of the draft genome and assembly of *Bacillus weihenstephanensis* KBAB4

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1011)

AUTHORS Larimer,F. and Land,M.

CONSRTM US DOE Joint Genome Institute (JGI-ORNL)

TITLE Annotation of the draft genome assembly of *Bacillus weihenstephanensis* KBAB4

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1011)

AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K., Detter,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E., Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S., Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J., Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S., Nuguen-the,C. and Sorokin,A.

CONSRTM US DOE Joint Genome Institute (JGI-PGF)

TITLE Direct Submission

JOURNAL Submitted (02-MAR-2006) US DOE Joint Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

COMMENT URL -- <http://www.jgi.doe.gov>  
Contact: Paul Richardson (microbes@cuba.jgi-psf.org)  
Draft sequencing done at US DOE Joint Genome Institute  
Source DNA and bacteria available from Alexei Sorokin (alexei.sorokine@jouy.inra.fr)  
The JGI and collaborators endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to follow them. It is our intention to publish the work of this

project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>)

Notes:

*Bacillus weihenstephanensis* KBAB4 was originally isolated from forest soil near Versailles, France, and was originally identified as *Bacillus cereus* (Vilas-Boas et al, Appl Env Microbiol, 2002, 68, 1414). More detailed phylogenetic analysis, using MLST, of the Versailles Collection of *B. cereus* and *B. thuringiensis* strains revealed that the strain grows at low temperature (6°C) and clusters with many other strains able to grow at low temperatures, including the independently isolated and characterized strains WSBC10204 and WSBC10206 (Sorokin et al, Appl Env Microbiol, 2006, 72, 1569). The latter two strains are the type strains of a newly recognized species in the *B. cereus* group able to grow in cold and having the species name *Bacillus weihenstephanensis* (Lechner et al, Int. J. Syst. Bacteriol, 1998, 48, 1373). Since, by MLST, KBAB4 is very closely related to WSBC10204 and represents many other psychrotrophic strains, it was assigned a species name *Bacillus weihenstephanensis* and the strain KBAB4 should also be considered as a type representative of this species.

FEATURES                      Location/Qualifiers

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ORIGIN

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Features:

 ☐ 1: [Z99117](#). Reports *Bacillus subtilis*...[gi:32468796]

Links

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LOCUS BSUB0014 1044 bp DNA linear BCT 18-APR-2005

DEFINITION *Bacillus subtilis* complete genome (section 14 of 21): from 2613658 to 2812830.

ACCESSION [Z99117](#) REGION: complement(21662..22705)

VERSION [Z99117.2](#) GI:32468796

KEYWORDS .

SOURCE *Bacillus subtilis* subsp. *subtilis* str. 168

ORGANISM *Bacillus subtilis* subsp. *subtilis* str. 168  
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1 (bases 1 to 1044)

AUTHORS Kunst,F., Ogasawara,N., Moszer,I., Albertini,A.M., Alloni,G., Azevedo,V., Bertero,M.G., Bessieres,P., Bolotin,A., Borchert,S., Borriss,R., Boursier,L., Brans,A., Braun,M., Brignell,S.C., Bron,S., Brouillet,S., Bruschi,C.V., Caldwell,B., Capuano,V., Carter,N.M., Choi,S.K., Codani,J.J., Connerton,I.F., Cummings,N.J., Daniel,R.A., Denizot,F., Devine,K.M., Dusterhoft,A., Ehrlich,S.D., Emmerson,P.T., Entian,K.D., Errington,J., Fabret,C., Ferrari,E., Foulger,D., Fritz,C., Fujita,M., Fujita,Y., Fuma,S., Galizzi,A., Galleron,N., Ghim,S.Y., Glaser,P., Goffeau,A., Golightly,E.J., Grandi,G., Guiseppi,G., Guy,B.J., Haga,K., Haiech,J., Harwood,C.R., Henaut,A., Hilbert,H., Holsappel,S., Hosono,S., Hullo,M.F., Itaya,M., Jones,L., Joris,B., Karamata,D., Kasahara,Y., Klaerr-Blanchard,M., Klein,C., Kobayashi,Y., Koetter,P., Koningstein,G., Krogh,S., Kumano,M., Kurita,K., Lapidus,A., Lardinois,S., Lauber,J., Lazarevic,V., Lee,S.M., Levine,A., Liu,H., Masuda,S., Mauel,C., Medigue,C., Medina,N., Mellado,R.P., Mizuno,M., Moestl,D., Nakai,S., Noback,M., Noone,D., O'Reilly,M., Ogawa,K., Ogiwara,A., Oudega,B., Park,S.H., Parro,V., Pohl,T.M., Portetelle,D., Porwollik,S., Prescott,A.M., Presecan,E., Pujic,P., Purnelle,B., Rapoport,G., Rey,M., Reynolds,S., Rieger,M., Rivolta,C., Rocha,E., Roche,B., Rose,M., Sadaie,Y., Sato,T., Scanlan,E., Schleich,S., Schroeter,R., Scoffone,F., Sekiguchi,J., Sekowska,A., Seror,S.J., Serror,P., Shin,B.S., Soldo,B., Sorokin,A., Tacconi,E., Takagi,T., Takahashi,H., Takemaru,K., Takeuchi,M., Tamakoshi,A., Tanaka,T., Terpstra,P., Tognoni,A., Tosato,V., Uchiyama,S., Vandenbol,M., Vannier,F., Vassarotti,A., Viari,A., Wambutt,R., Wedler,E., Wedler,H., Weitzenegger,T., Winters,P., Wipat,A., Yamamoto,H., Yamane,K., Yasumoto,K., Yata,K., Yoshida,K., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and Danchin,A.

TITLE The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*

JOURNAL Nature 390 (6657), 249-256 (1997)

PUBMED [9384377](#)

REFERENCE 2 (bases 1 to 1044)

AUTHORS Kunst,F., Ogasawara,N., Yoshikawa,H. and Danchin,A.

TITLE Direct Submission



JOURNAL Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur, Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48

COMMENT On Jul 7, 2003 this sequence version replaced gi:2634966. This entry contains data from release R16.1 of the SubtiList database. Further data on gene annotation and detailed information about changes from previous releases can be found at <http://genolist.pasteur.fr/SubtiList/>.

FEATURES Location/Qualifiers

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Range: from 2643434 to 2644498

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☐ Reverse complemented strand Fea☐ 1: CP000002. Reports *Bacillus lichenif...*[gi:56160984]

Links

Comment Features Sequence

LOCUS CP000002 1065 bp DNA linear BCT 03-DEC-2004

DEFINITION *Bacillus licheniformis* ATCC 14580, complete genome.

ACCESSION CP000002 REGION: 2643434..2644498

VERSION CP000002.2 GI:56160984

KEYWORDS .

SOURCE *Bacillus licheniformis* ATCC 14580 (DSM 13)

ORGANISM *Bacillus licheniformis* ATCC 14580  
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1 (bases 1 to 1065)

AUTHORS Rey,M.W., Ramaiya,P., Nelson,B.A., Brody-Karpin,S.D.,  
Zaretsky,E.J., Tang,M., de Leon,A.L., Xiang,H., Gusti,V.,  
Clausen,I.G., Olsen,P.B., Rasmussen,M.D., Andersen,J.T.,  
Jorgensen,P.L., Larsen,T.S., Sorokin,A., Bolotin,A., Lapidus,A.,  
Galleron,N., Ehrlich,S.D. and Berka,R.M.

TITLE Complete genome sequence of the industrial bacterium *Bacillus licheniformis* and comparisons with closely related *Bacillus* species

JOURNAL *Genome Biol.* 5 (10), R77 (2004)

PUBMED 15461803

REFERENCE 2 (bases 1 to 1065)

AUTHORS Berka,R.M., Rey,M.W. and Ramaiya,P.

TITLE Direct Submission

JOURNAL Submitted (14-JUL-2004) Novozymes Biotech Inc, 1445 Drew Ave,  
Davis, CA 95616, USA

REFERENCE 3 (bases 1 to 1065)

AUTHORS Berka,R.M., Rey,M.W. and Ramaiya,P.

TITLE Direct Submission

JOURNAL Submitted (29-SEP-2004) Novozymes Biotech Inc, 1445 Drew Ave,  
Davis, CA 95616, USA

REMARK Sequence update by submitter

COMMENT On Dec 1, 2004 this sequence version replaced gi:52001702.

FEATURES

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ORIGIN

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LOCUS BA000004 1029 bp DNA linear BCT 01-DEC-2004

DEFINITION *Bacillus halodurans* C-125 DNA, complete genome.

ACCESSION [BA000004](#) REGION: 1421231..1422259

VERSION BA000004.3 GI:47118318

KEYWORDS .

SOURCE *Bacillus halodurans* C-125

ORGANISM *Bacillus halodurans* C-125  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE 1

AUTHORS Takami, H.

TITLE Genome analysis of facultatively alkaliphilic *Bacillus halodurans* C-125

JOURNAL (in) Horikoshi, K. and Tsujii, K. (Eds.);  
EXTREMOPHILES IN DEEP-SEA ENVIRONMENTS: 249-284;  
Springer-Verlag (1999)

REFERENCE 2

AUTHORS Takami, H. and Horikoshi, K.

TITLE Reidentification of facultatively alkaliphilic *Bacillus* sp. C-125 to *Bacillus halodurans*

JOURNAL Biosci. Biotechnol. Biochem. 63, 943-945 (1999)

REFERENCE 3

AUTHORS Takami, H., Nakasone, K., Hiramata, C., Takaki, Y., Masui, N., Fuji, F., Nakamura, Y. and Inoue, A.

TITLE An improved physical and genetic map of the genome of alkaliphilic *Bacillus* sp. C-125

JOURNAL Extremophiles 3 (1), 21-28 (1999)

PUBMED [10086841](#)

REFERENCE 4

AUTHORS Takami, H., Nakasone, K., Ogasawara, N., Hiramata, C., Nakamura, Y., Masui, N., Fuji, F., Takaki, Y., Inoue, A. and Horikoshi, K.

TITLE Sequencing of three lambda clones from the genome of alkaliphilic *Bacillus* sp. strain C-125

JOURNAL Extremophiles 3 (1), 29-34 (1999)

PUBMED [10086842](#)

REFERENCE 5

AUTHORS Takami, H., Takaki, Y., Nakasone, K., Hiramata, C., Inoue, A. and Horikoshi, K.

TITLE Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic *Bacillus* sp. strain C-125

JOURNAL Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)

PUBMED [10192928](#)

REFERENCE 6

AUTHORS Takami, H., Masui, N., Nakasone, K. and Horikoshi, K.

TITLE Replication origin region of the chromosome of alkaliphilic *Bacillus halodurans* C-125

JOURNAL Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)

PUBMED [10427704](#)

REFERENCE 7  
AUTHORS Takami,H., Takaki,Y., Nakasone,K., Sakiyama,T., Maeno,G.,  
Sasaki,R., Hiramama,C., Fujii,F. and Masui,N.  
TITLE Genetic analysis of the chromosome of alkaliphilic Bacillus  
halodurans C-125  
JOURNAL Extremophiles 3 (3), 227-233 (1999)  
PUBMED [10484179](#)

REFERENCE 8  
AUTHORS Takami,H. and Horikoshi,K.  
TITLE Analysis of the genome of an alkaliphilic Bacillus strain from an  
industrial point of view  
JOURNAL Extremophiles 4 (2), 99-108 (2000)  
PUBMED [10805564](#)

REFERENCE 9  
AUTHORS Nakasone,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T.,  
Hiramama,C., Fujii,F. and Takami,H.  
TITLE Characterization and comparative study of the rrn operons of  
alkaliphilic Bacillus halodurans C-125  
JOURNAL Extremophiles 4 (4), 209-214 (2000)  
PUBMED [10972189](#)

REFERENCE 10  
AUTHORS Takami,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N.,  
Fujii,F., Hiramama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and  
Horikoshi,K.  
TITLE Complete genome sequence of the alkaliphilic bacterium Bacillus  
halodurans and genomic sequence comparison with Bacillus subtilis  
JOURNAL Nucleic Acids Res. 28 (21), 4317-4331 (2000)  
PUBMED [11058132](#)

REFERENCE 11 (bases 1 to 1029)  
AUTHORS Takami,H. and Takaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and  
Technology Center, Deep-sea Microorganisms Research Group; 2-15  
Natsushima, Yokosuka, Kanagawa 237-0061, Japan  
(E-mail:[takamih@jamstec.go.jp](mailto:takamih@jamstec.go.jp),  
URL:<http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html>,  
Tel:81-468-67-3895, Fax:81-468-66-6364)

COMMENT On or before Dec 8, 2004 this sequence version replaced  
[gi:10172612](#), [gi:10172890](#), [gi:10173176](#), [gi:10173440](#), [gi:10173727](#),  
[gi:10174030](#), [gi:10174345](#), [gi:10174613](#), [gi:12641879](#), [gi:10175192](#),  
[gi:10175500](#), [gi:10175792](#), [gi:10176109](#), [gi:10176401](#).

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## ORIGIN

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LOCUS AP006627 1023 bp DNA linear BCT 28-JUL-2006

DEFINITION *Bacillus clausii* KSM-K16 DNA, complete genome.

ACCESSION [AP006627](#) REGION: 1778796..1779818

VERSION AP006627.1 GI:56908016

KEYWORDS

SOURCE *Bacillus clausii* KSM-K16

ORGANISM *Bacillus clausii* KSM-K16  
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1

AUTHORS Hakamada,Y., Kobayashi,T., Hitomi,J., Kawai,S. and Ito,S.

TITLE Molecular cloning and nucleotide sequence of the gene for an alkaline protease from the alkalophilic *Bacillus* sp. KSM-K16

JOURNAL J. Ferment. Bioeng. 78, 105-108 (1994)

REFERENCE 2

AUTHORS Kobayashi,T., Hakamada,Y., Adachi,S., Hitomi,J., Yoshimatsu,T., Koike,K., Kawai,S. and Ito,S.

TITLE Purification and properties of an alkaline protease from alkalophilic *Bacillus* sp. KSM-K16

JOURNAL Appl. Microbiol. Biotechnol. 43 (3), 473-481 (1995)

PUBMED [7632397](#)

REFERENCE 3

AUTHORS Shirai,T., Suzuki,A., Yamane,T., Ashida,T., Kobayashi,T., Hitomi,J. and Ito,S.

TITLE High-resolution crystal structure of M-protease: phylogeny aided analysis of the high-alkaline adaptation mechanism

JOURNAL Protein Eng. 10 (6), 627-634 (1997)

PUBMED [9278275](#)

REFERENCE 4

AUTHORS Sakaki,Y., Kageyama,Y., Shimamura,S., Suzuki,H., Nishi,S., Hatada,Y., Kawai,S., Ito,S. and Horikoshi,K.

TITLE The complete genome sequence of the alkaliphilic *Bacillus clausii* KSM-K16

JOURNAL Unpublished

REFERENCE 5 (bases 1 to 1023)

AUTHORS Sakaki,Y., Kageyama,Y., Shimamura,S., Suzuki,H., Nishi,S., Hatada,Y., Kawai,S., Ito,S. and Horikoshi,K.

TITLE Direct Submission

JOURNAL Submitted (19-OCT-2003) Yasushi Kageyama, Kao Corporation, Biological Science Laboratories; 2606 Akabane, Ichikai-machi, Haga-gun, Tochigi 321-3497, Japan  
(E-mail:kageyama.yasushi@kao.co.jp, URL:http://www.kao.co.jp/e/, Tel:81-285-68-7516, Fax:81-285-68-7547)

FEATURES

source Location/Qualifiers

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CDS

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LEAYLDSPAQETVLVVVAPYEKLDERKKITKKLKKQTS AIDVNPFD EKETFAWMEAIA  
KQEGVAIEQDAKQLLYKRTGPNLMLLHRELEKCM LYSKDGPVTASIVDELVAETVEQ  
SVFTVIDYTAKGRAGDAVRLYHQLLRQKEEPLAILALLTRQFRQFFQVKTRLAKGYTQ  
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LRLAST"

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1021 taa

//

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[NCBI](#) | [NLM](#) | [NIH](#)

Aug 15 2006 13:27:38

## **Exhibit 2**

#####  
# Program: needle  
# Rundate: Wed Aug 23 05:38:23 2006  
# Align\_format: srspair  
# Report\_file: /ebi/extserv/old-work/needle-20060823-05382260401273.output  
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# Similarity: 1030/1047 (98.4%)  
# Gaps: 3/1047 ( 0.3%)  
# Score: 6325.0  
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#  
#=====

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SEQ_177	51	TTATTTATTATACGGCAATGAGCCGTTTTATTAAACGGAAACGTATGAGC	100
G_kaustophilu	51	ttatttattatacggcaatgagccgtttttattaacggaaacgtatgagc	100
SEQ_177	101	GATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACTTGGCT	150
G_kaustophilu	101	gattggtgaacgcagcgcttggccccgaggagcgggagtggaaacttggt	150
SEQ_177	151	GTGTACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGGCCGA	200
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G_kaustophilu	151	gtgtacgactgcgaggaaacgccggtcgaggcggcgcttgaggaggcca	200
SEQ_177	201	GACGGTGCCGTTTTTCGGCGAGCGGCGTGTCTCATCAAGCATCCAT	250
		.	
G_kaustophilu	201	gacggtgccgtttttcggcgagcggcggtgtcatcctcatcaagcatccat	250
SEQ_177	251	ATTTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTTGGCGAAG	300
		.	
G_kaustophilu	251	attttttcacgtctgaaaaagagaaggagatcgaacatgatttggcgaag	300
SEQ_177	301	CTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCTTTT	350
G_kaustophilu	301	ctggaggcgtacttgaaggcgccgctcgccgttttcgatcgtcgtctttt	350
SEQ_177	351	CGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCTCGCCA	400
G_kaustophilu	351	cgcgccgtacgagaagcttgatgagcgaaaaaaattacgaagctcgcca	400
SEQ_177	401	AAGAGCAAAGCGAAGTCGTCATCGCCGCCCCGCTCGCCGAAGCGGAGCTG	450
G_kaustophilu	401	aagagcaaagcgaagtcgtcatcgccgccccgctcgccgaagcggagctg	450
SEQ_177	451	CGTGCCTGGGTGCGGCGCCGCATCGAGAGCCAAGGGGCGCAAGCAAGCGA	500
		.	
G_kaustophilu	451	cgcgcctgggtgcgggcgccgcacgagagccaaggggcgcaagcaagcga	500



SEQ_177	501	CGAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGACGCAGCTTTCCGCCT	550
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G_kaustophilu	551	tggcgaatgaaatcgataaattggccctgtttgccggatcgggcggaacc	600
SEQ_177	601	ATCGAGGCGGCGGCGGTTGAGCGGCTTGTCGCCCCGCACGCCGGAAGAAAA	650
G_kaustophilu	601	atcgaggcggcggcggttgaacggcttgctgcggcgacgccggaagaaaa	650
SEQ_177	651	CGTATTTGTGCTTGTCGAGCAAGTGGCGAAGCGCGACATTCCAGCAGCGT	700
G_kaustophilu	651	cgtatTTGTGCTTGTCGAGCAAGTGGCGAAGCGCGACATTCCAGCAGCGT	700
SEQ_177	701	TGCAGACGTTTTATGATCTGCTTGAAAACAATGAAGAGCCGATCAAAATT	750
G_kaustophilu	701	tgcagacgTTTTATGATCTGCTTGAAAACAATGAAGAGCCGATCAAAATT	750
SEQ_177	751	TTGGCGTTGCTCGCCGCCCATTTCCGCTTGCTTTCGCAAGTGAAATGGCT	800
G_kaustophilu	751	ttggcgctgctcgccgcccatTTCCGCTTGCTTTCGCAAGTGAAATGGCT	800
SEQ_177	801	TGCCTCCTTAGGCTACGGACAGGCGCAAATTGCTGCGGCGCTCAAGGTGC	850
G_kaustophilu	801	tgccctccttaggctacgggacaggcgcaaattgctgcggcgctcaaggtgc	850
SEQ_177	851	ACCCGTTCCGCGTCAAGCTCGCTCTTGCTCAAGCGGCCCGCTTCGCTGAC	900
G_kaustophilu	851	acccgTTCCGCGTCAAGCTCGCTCTTGCTCAAGCGGCCCGCTTCGCTGAC	900
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SEQ_177	951	GAAAAGCGGGGCGGTGATCGCCGGTTGGCCGTTGAGCTGCTTCTGATGC	1000
G_kaustophilu	951	gaaaagcggagcggtcgatcgccggttgggcggttgagctgcttctgatgc	1000
SEQ_177	1001	GCTGGGGCGCCCCGCGCGCAAGCGGGGCGCCACGGCCGGCGG	1044
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SEQ_177	97	GAGCGATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAAGTT	146
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Bacillus_sp_N	97	cagctgcttatcaacaatgtgctgg---ctgaaga-cgagagcgatttta	142
SEQ_177	147	GGCTGTGTACGACTGC----GAGGAAACGCCGATCGAGGCGGCGCTTGAG	192
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Bacillus_sp_N	143	atctgtctacatatgatttggaggaaacaccaatagaagcggcacttgag	192
SEQ_177	193	GAGGCCGAGACGGTGCCGTTTTTCGGCG---AGCGGCGTGTCTATTCTCAT	239
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Bacillus_sp_N	193	gatgcagagaccttccctttcatgggggataagaggctcatctttcttca	242
SEQ_177	240	CAAGCATCCATATTTTTTTTACGTCTGAAAA---AGAGAAGGAGATCGAAC	286
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Bacillus_sp_N	243	caa-c---ccctcttttctgacttccgaaaagacaaaggggaagactgagc	289
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SEQ_177	337	ATCGTCGTCTTTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAAT	386
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Bacillus_sp_N	340	attattgtgtttgcggcaccctatgaaaagctggatgatagaaaaaagat	389
SEQ_177	387	TACGAAGCTCGCCAAAGAGCAAAGCGAAGTCGTTCATCGCCGCC---CCGC	433
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Bacillus_sp_N	390	tacgaag-gaactgaagaaaaaagc-aagt-gtccttgaggccaaaaaac	436
SEQ_177	434	TCGCCGAAGC-GGAGCTGCGTGCCTGGGTGCGGCGCCGCATCGAGAGCCA	482
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Bacillus_sp_N	437	t-gggggagcaggagctgaaagtctggatcagg---gaaagggctgccc	481

SEQ_177	483	AGG--GGCG-CAAGCAAGCGACGAGGCGATTGATGTCCTG---TTGCGG-	525
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SEQ_177	526	--CGGGCCGGGAC--GCAGCTTTCCGCCTTGGCGAATGAAATCGATAAAT	571
Bacillus_sp_N	527	ctctggcaggtaccaacctctttatgc--tgacaggtgaaattgataaat	574
SEQ_177	572	TGGCCCTGTTTGCCGGATCGGGCGGAACC--ATCGAGGCGGCGGCGGTTG	619
Bacillus_sp_N	575	tggccttatatgccg--acgaggaaaagctgattgatgccgaggcagttg	622
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SEQ_177	820	CAGGCGCAAATTGCTGCGGC-GC-TCAAGGTGCACCCGTTCCGCGTCAAG	867
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SEQ_177	868	CTCGCTCTTGCTCAAGCGGCCCGC--TTCGCTGACGGAGAGCTTGCTGAG	915
Bacillus_sp_N	871	cttgcagccggacaggc--ccagcttttcggagatgaagaactgtcc---	915
SEQ_177	916	GCG-ATCAACGAGC-TC--GCTGACGCCGATTACGAAGTGAAAAGCGGGG	961
Bacillus_sp_N	916	-cgcatcatgaagcttctggcagaagcagattatgagatgaaaa-caggg	963
SEQ_177	962	CGGTCGATCGCCGGTTGGC-CGTTGAGCTGCTTCTGATGCGCTGGGCGC	1010
Bacillus_sp_N	964	gggatgaacaaggaaatgcttattgagatgtttttgtt---cag---gc	1006
SEQ_177	1011	CCGCCCGGCGCAAGCGGGCGCCAC-GGCCGGCGG	1044
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# Extend_penalty: 0.5
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# Length: 1072
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# Similarity: 582/1072 (54.3%)
# Gaps: 89/1072 ( 8.3%)
# Score: 2732.0
#
#
#=====

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B_cereus_subs 1 atgagtgatatacataag----aaaattaaaaagaacagtttgctccgt      46

SEQ_177      50 TTTATTTTATTATACGGCAATG-AGCCGTTTTTTATTAACGGAAACGTATGA      98
      ||||| |||||.|||.|||.|||. |||||.|||.|||.|||. |||||. |
B_cereus_subs 47 tttattttattgtatggaacggaagcctattttataaat-gaaac----aa      91

SEQ_177      99 GCGATTGGTGAAC----GCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAAC      144
      .|||.|||.|||.|||. |. |||.|||.|||.|||.|||.|||.|||.
B_cereus_subs 92 tcgattttaattacagtagaggcacttgccgaagaagatcgtgattttaat      141

SEQ_177      145 TTGGCTGTGTACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGA      194
      .|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
B_cereus_subs 142 attgttacatatgatttagaagaggcgtatttagaggatgtagtagagga      191

SEQ_177      195 GGCCGAGACGGTGCCGTTTTTCGGCGAGCGGCGTGTTCATTCTCATCAAGC      244
      .|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
B_cereus_subs 192 tgcaaggacgcttccattctttggagagcgaaaaatattattaataaagt      241

SEQ_177      245 ATCCATATTTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTTG      294
      ..|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
B_cereus_subs 242 ccccgttatttttaacatcacagaaagaaaaattg---gagcaaatata      288

SEQ_177      295 GCGAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGT      344
      ...|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
B_cereus_subs 289 aaaatccttgaggaatatattgctgaaccatctccattttcgatcatgat      338

SEQ_177      345 CTTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGC      394
      .|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
B_cereus_subs 339 ttttatcgctccatatgaaaagttagatgagcgaaaaaaattacgaag-      387

SEQ_177      395 TCGCCAAAGAGCAAAGC-GAAGTCGTCATCGC---CGCCCCGCTCGCCGA      440
      |....|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
B_cereus_subs 388 ttattaaagaaaacggctgaggtagtagaagcgaaatgctatgcaagtaca      437

SEQ_177      441 AGCGGAGCTGCGTGCCTGGGTGCGGCGCCGCATCGAGAGCC-AAGGGGCG      489
      |||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
B_cereus_subs 438 agatg---ttaggaaatggat-----tgtaaagcgtgctgaagaagtt      477
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SEQ_177	534	GACGCAGCTTTCCGCC-TTGGCGAATGAAATCGATAAATTGGCCCTGTTT	582
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B_cereus_subs	528	ga-gcaatgtaacaatgtagcaaaggaaatggataagttaacactgtat	576
SEQ_177	583	GCCGGATCGGGCGGAACCATCGAGGCGGCGGCGGTTGAGCG--GCTTGT	629
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B_cereus_subs	577	gttggaacgggaggagacatt---acaacaaaacttgtaagtgaacttgt	623
SEQ_177	630	CGCCCGCACGCCG--GAAGAAAACGTATTTGTGCTTGTC-GAGCAAGTGG	676
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SEQ_177	677	CGAAGCGCGACATTCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAA	726
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B_cereus_subs	671	taaaaaaagatatagcaggagcaatgaaaatattagatggcttatttaca	720
SEQ_177	727	AACAATGAAGAGCCGATCAAAATTTTGGCGTTGCTCGCCGCCCATTTCCG	776
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B_cereus_subs	721	caacaggaagaaccaattaaattattagcgttgctagtgaagtcaattccg	770
SEQ_177	777	CTTGCTTTTCGCAAGTGAAATGGCT--TGCCTCCTTAGGCTACGGACAGGC	824
		.   .   .   .   .   .   .   .   .   .   .   .	
B_cereus_subs	771	tttattacatcaagtaaaagaactacagcagc--gaggatacggacaaaa	818
SEQ_177	825	GCAAATTGCTGCGGCGCTCAAGGTG--CACCCGTTCCGCGTCAAGCTCGC	872
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B_cereus_subs	819	tcaaattgcttc-gc-atattggtgttcacccgtaccgagtaaaattggc	866
SEQ_177	873	TCTTGCTCAAGCGGCCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATCA	922
		..   .   .   .   .   .   .   .   .   .   .   .	
B_cereus_subs	867	gatgaatcaaacgaaacttttctcatttgaagaattgaaaaaggtaattt	916
SEQ_177	923	ACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGGGCGGTCGATCGC	972
		.     .   .   .   .   .   .   .   .   .   .   .	
B_cereus_subs	917	tcgagtttagcggaagcggactatagtatgaaaacagggaaaatggataag	966
SEQ_177	973	CGGTTGGCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCCGGCGCA	1022
		..   .   .   .   .   .   .   .   .   .   .   .	
B_cereus_subs	967	aagttagttctagaatttttcttaatg-----agactgaatca	1004
SEQ_177	1023	AGCGGGGCGCCACGGCCGGCGG	1044
		... . . .	
B_cereus_subs	1005	tatgtga	1011



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# Rundate:  Wed Aug 23 14:53:14 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work
#####
```

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# Aligned_sequences: 2
# 1: SEQ_177
# 2: B_anthraxis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1066
# Identity:      585/1066 (54.9%)
# Similarity:    585/1066 (54.9%)
# Gaps:          77/1066 ( 7.2%)
# Score: 2717.0
#
#
#=====
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SEQ_177	1	ATGC-TGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTTCTCCTCCC	49
		.   ..  ..  . .   .   .     ..  ..   .     ..	
B_anthraxis	1	atgagtgatatacata----aaaagattaaaaaaaaagcagtttgctccgt	46
SEQ_177	50	TTTATTTATTATACGGCAATGAGCCGTTTTTTATTAACGGAAACGTATGAG	99
		.       .   .   .  ..   .       .     .     .....	
B_anthraxis	47	tgtatttactgtatggaacggaagcggttttttataaatgaaacgataaag	96
SEQ_177	100	CGATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACTTGGC	149
		... ... .. .       ..... ..   .   .     .   .  .	
B_anthraxis	97	cttattacaacagaagcgcttgaagaggaagatcgcgagtttaat---gt	143
SEQ_177	150	TGTG---TACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGG	196
		..   .  ..   .     .  .... .   .   .   .       .	
B_anthraxis	144	tgtgacatatgatttagaagaagcggtatttagaagatgtggttgaggatg	193
SEQ_177	197	CCGAGACGGTGCCGTTTTTTCGGCGAGCGGCGTGTTCATTCTCATCAAGCAT	246
		....   .   .       ..   .   .... ..   .   .   .  ....	
B_anthraxis	194	cacgtacacttccttttttcggagaacgtaaagtgttattaataaaaatca	243
SEQ_177	247	CCATATTTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTTGGC	296
		.     .     .   .       .    ..   .     .   .  ....	
B_anthraxis	244	ccattatttttaacgtcacaaaaagaaa--agttagaacaaaatataaa	290
SEQ_177	297	GAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCT	346
		. ... .   .  ..  ..  ..   .   .   .     .  ..   .   .	
B_anthraxis	291	aatttttagaagaatatatcggggaaccttctccattttctattcttgttt	340
SEQ_177	347	TTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCTC	396
		.     .     .       ..   .       ..   .   .	
B_anthraxis	341	ttgttgcgcccttacgaaaagccttgatgaacgaaaaaaattacaaaact-	389
SEQ_177	397	GCCAAAGAGCAAAGC-GAAGTCGTCATCGCCGCCCGCTCGCCGAAGCGG	445
		...     .   .      .. .  .... .....   .     ....   .	
B_anthraxis	390	attaaagaaaacagcagatatagtagaagcgaatgcgat-gcaagtgcag	438
SEQ_177	446	AGCTGCGTGCCTGGGTGCGGCGCCGCATCGAG-AGCCAAGGGGC---GC	490
		.      .  ....   ....  ..      .     .... .      .	
B_anthraxis	439	-gat--gttcaaaaagtggattgtagc-tcgtgcagaggaagggcatgtac	484

SEQ_177	491	AAGCAAGCGACGAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGACGCAG	540
		..... .. ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	485	atattgataatgcagctgttagtttattgtagagcttg-tgggaagtaa	533
SEQ_177	541	CTTTCCGCC- TTGGCGAATGAAATCGATAAATTGGCCCTGTTTGCCGGAT	589
		.. .. ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	534	tgtgacgatgttggcgaaggaaatggacaagttaacgttatacgtcggta	583
SEQ_177	590	CGGGCGGAACCATCGAGGCGGCGGCGGTTGAGCGGCTTGTCGCCCCGCAGC	639
		. ... ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	584	tgggcggagagattacgccgaaacttgttgcagagcttgt-gccaaaat-	631
SEQ_177	640	CCG--GAAGAAAACGTATTTGTGCTTGTGCGAGCAAGTGGCGAAGCGCGAC	687
		. ... ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	632	cagttgaacaaaatgtatttgccttaacagaaaaagtggtaaaaaaagat	681
SEQ_177	688	ATTCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAAAACAATGAAGA	737
		.. ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	682	atcgcaggtgcgatgcaaattttggatggattatttacgcagcaggagga	731
SEQ_177	738	GCCGATCAAAATTTTGGCGTTGCTCGCCGCCCATTTCCGCTTGCTTTCGC	787
		. ... ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	732	accgattaaattgcttgcgttgtagtaagtcaattccgcttgctgcac	781
SEQ_177	788	AAGTGAAATGGCTTGCCCTC--CTTAGGCTACGGACAGGCGCAAATTGCTG	835
		... ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	782	aagtaaaagag-ttacagcagcgt-ggttatggacaaaatcaaattgct-	828
SEQ_177	836	CGGCGCTCA---AGGTG--CACCCGTTCCGCGTCAAGCTCGCTCTTGCTC	880
		. ... ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	829	----tctcatattggtgtacatccatatcgtgtaaagttagcgatgaatc	874
SEQ_177	881	AAGCGGCCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATCAACGAGCTC	930
		.. ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	875	aaacgaagtttttctcttttgaagaactaaaaaagtgattatagaattg	924
SEQ_177	931	GCTGACGCCGATTACGAAGTGAAAAGCGGGGCGGTTCGAT-CGCCGGTTG-	978
		.. ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	925	gcggaagctgattatagtatgaagactggaaaaatggataagaaacttgt	974
SEQ_177	979	GCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCCGGCGCAAGCGGG	1028
		... ... ... ... ... ... ... ... ... ... ... ...	
B_anthraxis	975	gc--ttgagtttttcttaatgcgat-----taaatcatatgtga	1011
SEQ_177	1029	GCGCCACGGCCGCGG	1044
B_anthraxis	1012		1011

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# Program: needle  
# Rundate: Wed Aug 23 15:01:17 2006  
# Align_format: srspair  
# Report_file: /ebi/extserv/old-work/needle-20060823-15011448417323.output  
#####  
  
#=====  
#  
# Aligned_sequences: 2  
# 1: SEQ_177  
# 2: B_cereus  
# Matrix: EBLOSUM62  
# Gap_penalty: 10.0  
# Extend_penalty: 0.5  
#  
# Length: 1076  
# Identity: 588/1076 (54.6%)  
# Similarity: 588/1076 (54.6%)  
# Gaps: 97/1076 ( 9.0%)  
# Score: 2650.0  
#  
#  
#=====
```

SEQ_177	1	ATGC-TGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTTCTCCCC	49
		.     .   .   .     .       .       .       .	
B_cereus	1	atgagtgatatacata----aaaagattaaaaagaagcagtttgctccgt	46
SEQ_177	50	TTTATTTATTATAACGGCAATGAGCCGTTTTTATTAAACGGAAACGTATGAG	99
		.           .         .     .     .           .       .           .	
B_cereus	47	tatat ttactatatggaaacagaagcg ttttttataaatgaaacgataaag	96
SEQ_177	100	CGATTGGTGAAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAAC TTGGC	149
		. .   . . .   . .             . . . .   .     .       .     .   .	
B_cereus	97	cttattacaacagaagcgcttgaagaggaagatcgcgagtttaat---gt	143
SEQ_177	150	TGTG---TACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGG	196
		.     .     .     .       .   . . . .   .     .   .           .	
B_cereus	144	tgtgacatatgat ttagaagaagcatat ttagaagatgtggttgaggatg	193
SEQ_177	197	CCGAGACGGTGCCGT TTTTCGGCGAGCGGCGTGTCATTCTCATCAAGCAT	246
		. . .     .   .               .     .     .     .     .     .   . . .	
B_cereus	194	cacgtacacttccttttttcggagaacgtaaagtgttattaataaaatca	243
SEQ_177	247	CCATATTT TTTTACGTCTGAAAAGAGAAGGAGATCGAACATGATTTGGC	296
		. .         .     .     .             .   .     .         .     .   . .	
B_cereus	244	ccactc tttttaacttcacaaaaagaaa-- agttagaacaaaatataaa	290
SEQ_177	297	GAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGT TTTTCGATCGTCGTCT	346
		.   . .   .     .   .       .   . .     .     .     .           .     .     .	
B_cereus	291	aatttttagaagaatatattggggaaaccttctcccttttctattcttgttt	340
SEQ_177	347	TTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAAAATTACGAAGCTC	396
		.   .         .         .         .                             .     .	
B_cereus	341	ttgttg cgccttacgaaaagctggatgaacgaaaaaaaaattacaaaact-	389
SEQ_177	397	GCCAAAGAGCAAAGC-GAAGTCGTCATCGC---CGCCCCGCTCGCCGAAG	442
		. . .           .   .           .     .     .     .     .     .     .	
B_cereus	390	attaaagaaaacagcg gatgtagtagaagcgaatgcaatgcaagtgcagg	439
SEQ_177	443	CGGAGCTG-CGTGCCTGGGTG--CGGCGCCGCATCGAGAGCCAAGGGGCG	489
		. .   . .   .   .       .   .   .   .     .	
B_cereus	440	atgttcagaagtggattgttgctcgg-gcag-atgaagtgc--atgtgca	485

SEQ_177	490	CA---AGCAAGCGACGAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGAC	536
B_cereus	486	tattgatcatgc-----ggctgttagtttgtttagagcttg-tgggaa	529
SEQ_177	537	GCAGCTTTCCGCC-TTGGCGAATGAAATCGATAAAATTGGCCCTGTTTGCC	585
B_cereus	530	gtaatgtaacgatgttggcgaaggaaatggacaagttaacgttatatgtc	579
SEQ_177	586	GGATCGGGCGGA-----ACCATCGAGGCGGCGGCGGTTGAGCGGCTTGTC	630
B_cereus	580	ggtatgggcgagatattacaccgaaac----tc-gttgcagagcttgt-	623
SEQ_177	631	GCCCGCACGCCG--GAAGAAAACGTATTTGTGC-TTGTC-GAGCAAGTGG	676
B_cereus	624	gccaaaat-cagttgaacaaaatgtgtt--tgctttgacagaaaaagtgg	670
SEQ_177	677	CGAAGCGCGACATTCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAA	726
B_cereus	671	taaaaaaagatatcgcggtgcatgcaaattttggatggattatttacg	720
SEQ_177	727	AACAATGAAGAGCCGATCAAAATTTTGGCGTTGCTCGCCGCCCATTTCCG	776
B_cereus	721	cagcaggaggaacctattaaattgcttgcgcttattagtaagtcaattccg	770
SEQ_177	777	CTTGCTTTTCGCAAGTGAAATGGCTTGCTC--CTTAGGCTACGGACAGGC	824
B_cereus	771	tttactgcatcaagtgaagag-ttacagcagcgt-ggttacggtcaaaa	818
SEQ_177	825	GCAAATTGCTGCGGCGC--TCAAGGTGCACCCGTTCCGCGTCAAGCTCG	871
B_cereus	819	tcaaatt--c-gcgtctcatattggtgtgcatccatctgtgtaaaattag	865
SEQ_177	872	CTCTTGCTCAAGCGGCCCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATC	921
B_cereus	866	cgatgaatcaaacgaagtttttctcttttgaagaattaaaaaaagtgata	915
SEQ_177	922	AACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGG-GCGGTCGAT-	969
B_cereus	916	atggaattagcgggaagctgattatagtatgaaaa-cgggaaaaaatggata	964
SEQ_177	970	CGCCGGTTG-GCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCCGG	1018
B_cereus	965	agaaacttgtgc--tcgagtttttcttaatgcggt-----taaat	1002
SEQ_177	1019	CGCAAGCGGGGCGCCACGGCCGGCGG	1044
B_cereus	1003	catatgtga	1011

#####

0000	0001	0002	0003	0004	0005	0006	0007	0008	0009	0010	0011	0012	0013	0014	0015	0016	0017	0018	0019	0020	0021	0022	0023	0024	0025	0026	0027	0028	0029	0030	0031	0032	0033	0034	0035	0036	0037	0038	0039	0040	0041	0042	0043	0044	0045	0046	0047	0048	0049	0050	0051	0052	0053	0054	0055	0056	0057	0058	0059	0060	0061	0062	0063	0064	0065	0066	0067	0068	0069	0070	0071	0072	0073	0074	0075	0076	0077	0078	0079	0080	0081	0082	0083	0084	0085	0086	0087	0088	0089	0090	0091	0092	0093	0094	0095	0096	0097	0098	0099
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

SEQ_177	1	ATGC-TGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTCTCCCC	49
		.   ..  ..    .   .   .    .... ..   .    ..	
B_thuringiens	1	atgagtgatatacata----aaaaaattaaaaagaaacagtttgctccgt	46
SEQ_177	50	TTTATTTATTATACGGCAATGAGCCGTTTTTTATTAACGGAAACGTATGAG	99
		.       .     .  ..  .. .     ..   ..     ....	
B_thuringiens	47	tataattactatatatgggacggaagctttttttataaatgaaacgataaag	96
SEQ_177	100	CGATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACCTTGGC	149
		... ... .. .   .     ....   .   .     ..   .  .	
B_thuringiens	97	cttattacgacagaagcacttgaagaagaagatcgagagtttaat---gt	143
SEQ_177	150	TGTG---TACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGG	196
		.     .  ..   .   .  .... .   .  .. . .	
B_thuringiens	144	tgtgacatacgaatttggagaagcgtatttagaagatgtggttgaggatg	193
SEQ_177	197	C-CGAGACGGTGCCGTTTTTTCGGCGAGCGGCGTGTTCATTCTCATCAAGCA	245
		.    . .   .   .   .       ....  .. .. .   .  ...	
B_thuringiens	194	cgcgt-acgcttcctttctttggagagcggaaagtactgttaataaaatc	242
SEQ_177	246	TCCATATTTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTG	295
		.  ....     .   .  ..       .      .   .  ..   .  ..	
B_thuringiens	243	accgctatttttgacttcgcaaaaagaaa---agttagagcaaaatataa	289
SEQ_177	296	CGAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTC	345
		.. ... .   .  ..   .  .... ..   .   .     .  .. .   .	
B_thuringiens	290	aaatttttagaagaatacattgggtgaaccttctccattttctattcttgtt	339
SEQ_177	346	TTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCT	395
		. .     .     .   .                       .  .	
B_thuringiens	340	tttggttgcgcccttacgaaaaacttgatgagcgaaaaaaattacaaaact	389
SEQ_177	396	CGCCAAAGAGCAAAGCGAAGTCGTCATCGCCGCCCGCTCGCCGAAGC-G	444
		...     .. .      ..  .. .  ..    ...     .    .	
B_thuringiens	390	-attaaagaaaacagc--agatgtagtagaag---cgaatg-cgatgcaa	432
SEQ_177	445	GAGCTGCGTGCCTGGGTGCGGC--GCCGCATCGAG-AGCCAAGGGGCGCA	491
		.   .  ..  ....  .. .  .  ..      .     .... .   ...	
B_thuringiens	433	gtgcaggatgttcagaagtggattgttgc-tcgggcagatgaagtgcattg	481



SEQ_177	492	AGCA-AGCGACGAGGCGATTGATGTCCTGTTGC---GGCGGGCCGGGACG	537
		.     ..  .. ..  ..  .. ...     ..    ..  ..	
B_thuringiens	482	tgcacattgataacgcggctgttagtttgctagagctgg-tgggaag	530
SEQ_177	538	CAGCTTTCGCC- TTGGCGAATGAAATCGATAAATTGGCCCTGTTTGCCG	586
		. ... ..  ..      ..   ..  ..  .. .. .. .. ..	
B_thuringiens	531	taatgtaacgatgttggcgaaggaaatggacaagttaacgttatagcttg	580
SEQ_177	587	GATCGGGCGGAACCATCGAGGCGGCGGCGGTTGAGCGGCTTGTCGCCCCG	636
		...   ... ... ... ... ... ... ... ... ... ...	
B_thuringiens	581	gtatgggaggagagattacaacgaaacttggtgcagagcttgt-gccaaa	629
SEQ_177	637	ACGCCG--GAAGAAAACGTATTTGTGC-TTGTG-CAGCAAGTGGCGAAGC	682
		.  .     ..   ..	
B_thuringiens	630	at-cagttgagcaaatgtatt--tgctttgacagaaaaagtggtagaaa	676
SEQ_177	683	GCGACATTCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAAAACAAT	732
		..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..	
B_thuringiens	677	aagatattgcaggtgcgatgcaaatgttggtgagattattacgcagcag	726
SEQ_177	733	GAAGAGCCGATCAAAATTTTGGCGTTGCTCGCCGCCCATTTCCGCTTGCT	782
		..   ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..	
B_thuringiens	727	gaagaaccgattaaattgcttgcatatttagtgagtcaattccgtttgtt	776
SEQ_177	783	TTCGCAAGTGAAATGGCTTGC--CTCCTTAGGCTACGGACAGGCGCAAAT	830
		. ..   ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..	
B_thuringiens	777	gtatcaagtgaagag-ttacagcaacgt-gggtatgggcaaatcaaat	824
SEQ_177	831	TGCTGCGGCGCTCAAGGTGCACCCGTTCCGCGTCAAGCTCGCTCTTGCTC	880
		.. ... ... ... ... ... ... ... ... ... ... ...	
B_thuringiens	825	tgcacacatattggtgtacatccgtatcgtgtaaaattggcaatgaatc	874
SEQ_177	881	AAGCGGCCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATCAACGAGCTC	930
		..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..	
B_thuringiens	875	aaacgaaatttttctcttttgaagaattaaaaaaagtgattatagaatta	924
SEQ_177	931	GCTGACGCCGATTACGAAGTGAAAAGCGGG-GCGGTCGAT-CGCCGTTG	978
		..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..	
B_thuringiens	925	gcggaagctgattatagtagaaga-cgggaagatggataagaaacttg	973
SEQ_177	979	-GCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCCGCGCAAGCGG	1027
		..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..	
B_thuringiens	974	tgc--tcgagtttttcttaatgcgat-----taaatacatatgtga	1011
SEQ_177	1028	GGCGCCACGGCCGGCGG	1044
B_thuringiens	1012		1011

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# Program:   needle
# Rundate:   Wed Aug 23 15:13:23 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060823-15132265139353.output
#####
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#
# Aligned_sequences: 2
# 1: SEQ_177
# 2: B_weihenstephanensis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1074
# Identity:      579/1074 (53.9%)
# Similarity:    579/1074 (53.9%)
# Gaps:          93/1074 ( 8.7%)
# Score: 2650.5
#
#
# =====
```

SEQ_177	1	ATGC-TGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTCTCCCC	49
B_weihensteph	1	atgagtgatatacataagaag----attaaaaagaacagttcgctccgt	46
SEQ_177	50	TTTATTTATTATACGGCAATGAGCCGTTTTTTATTAACGGAAACGTATGAG	99
B_weihensteph	47	tgtatgtactgtatggaacggaagccttattttataaatgaaacgataaag	96
SEQ_177	100	CGATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACCTTGGC	149
B_weihensteph	97	cttattacaacggaagcgcttgaagaggaagatcgagagtttaat---gt	143
SEQ_177	150	TGTG---TACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGG	196
B_weihensteph	144	tgtgacatacgaatttgaagaagcgtatttagaagatgtagttgaggatg	193
SEQ_177	197	CCGAGACGGTGCCGTTTTTTCGGCGAGCGGCGTGTTCATTCTCATCAAGCAT	246
B_weihensteph	194	cgcatacgccttccttttttggagagcgtaaagttatattaataaaaatca	243
SEQ_177	247	CCATATTTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTGGC	296
B_weihensteph	244	ccactatttttaacggcacaaaaagaaa--aattagaacaaaatataaa	290
SEQ_177	297	GAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCT	346
B_weihensteph	291	aatttttagaagaatatattggggagccatctcctttttctattccttgttt	340
SEQ_177	347	TTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCTC	396
B_weihensteph	341	ttgttgcgcccttatgaaaaattagacgaacgaaaaaaaaattacaaaact-	389
SEQ_177	397	GCCAAAGAGCAAAGCGAAGTCGTCATCGCCGCCCCGCTCGCCGAAGC-GG	445
B_weihensteph	390	attaaagaaaacagcg--gatgtaatagaag---caaatg-cgatgcaag	433
SEQ_177	446	AGCTGCGTGCCCTGGGTGCGGCGCCGCATCGAGAGC-CAAGGGGCGCAAGC	494
B_weihensteph	434	tgcaggatgttcagaagtgg-attgtttctcgtgcggatgaggtgcatg-	481

SEQ_177	495	AAGC-----GACGAGGCATTGATGTCTTTCGGCGGGCCGGGAC	536
B_weihensteph	482	-tgcataattgataatgcagctgttagtttatgttagagcttg-tgggaa	529
SEQ_177	537	GCAGCTTTCCGCC-TTGGCGAATGAAATCGATAAAATTGGCCCTGTTTGCC	585
B_weihensteph	530	gcaatgtaacaatgttggcgaaggaaatggacaagttaaactgtacgtc	579
SEQ_177	586	GGATCGGGCGGAACCATCGAGGCGGCGGCGGTTG-AGCGG--CTTGTCGC	632
B_weihensteph	580	ggtatggcgaggagaaatt---acgccaaaacttgtcacggaacttgt--g	624
SEQ_177	633	CCGCACGCCG--GAAGAAAACGTATTTGTGCTTGTTCGAGCAAGTGGCGAA	680
B_weihensteph	625	ccgaaatctgttgagcaaacgtgtttgctttaacagaaaaagtggtgaa	674
SEQ_177	681	GCGCGACATTCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAAAAACA	730
B_weihensteph	675	aaaagatatcgctgggtgcgatgcaa--ttttaga-cggattatttaca	720
SEQ_177	731	----ATGAAGAGCCGATCAAATTTTGGCGTTGCTCGCCGCCCATTTCCG	776
B_weihensteph	721	cagcaggaagaaccgattaaactgctcgctttatttagtaagtcagttccg	770
SEQ_177	777	CTTGCTTTTCGCAAGTGAAATGGCTTGCCTC--CTTAGGCTACGGACAGSC	824
B_weihensteph	771	cttgctgcatcaagtgaagag-ttgcaacagcgt-ggttacggacaaaa	818
SEQ_177	825	GCAAATTGCTGCGGCGCTCAAGGTG--CACCCGTTCCGCGTCAAGCTCGC	872
B_weihensteph	819	tcaaatcgcgtc--ccatattggtgtacatccgtaccgggtaaagtggc	866
SEQ_177	873	TCTTGCTCAAGCGGCCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATCA	922
B_weihensteph	867	gatgaatcaaacgaagtttttctcttttgaagaattaaanaaagtatta	916
SEQ_177	923	ACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGGGCGGTCGAT-CG	971
B_weihensteph	917	tagaattggcggaagctgattatagtagtaagactggaaagatggataag	966
SEQ_177	972	CCGGTTG-GCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCC GCCGCG	1020
B_weihensteph	967	aaacttgtgc--ttgagttttcttaaatgcggt-----taaatca	1004
SEQ_177	1021	CAAGCGGGGCGCCACGGCCGGCGG	1044
B weihensteph	1005	tatgtag	1011

```
# Program: needle
# Rundate: Wed Aug 23 15:18:12 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060823-15181247653341.output
#####
```

```
#
# Aligned_sequences: 2
# 1: SEQ_177
# 2: B_subtilis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1085
# Identity:      602/1085 (55.5%)
# Similarity:    602/1085 (55.5%)
# Gaps:          82/1085 ( 7.6%)
# Score: 2814.0
#
#
#=====
```

SEQ_177	1	ATGCTGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTC-TCCCC	49
B_subtilis	1	atggtatttgatgtgtggaaaagcc-tgaaaaaaggagaggtccatccgg	49
SEQ_177	50	TTTATTTATTATAACGGCAATGAGCCGTTTTTTATT-AACGGAAACGTATGA	98
B_subtilis	50	tttattgtttatacggaaaagagacatatctgctgcaagaaaccgtcagc	99
SEQ_177	99	GCGATTGGTGA-ACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGA ACTTG	147
B_subtilis	100	aggatcagacagacg-gtcg-ttgatcaggagacaaaaggatttcaatctg	147
SEQ_177	148	GCTGTGTACGA-CTG--CGAGGAAACGCC-GATCGAGGCGGCGCTTGAGG	193
B_subtilis	148	tccgtttttgatctggaagaggacctcgctggatcaa---gcgattgcag	193
SEQ_177	194	AGGCCGAGACGGTGCCGTTTTTTCGGCGAGCGGCG--TGTCATTCTCATC	240
B_subtilis	194	atgctgaaacgtttccgtttatgggggagcggcgtcttgtcatt---gtg	240
SEQ_177	241	AAGCATCCATATTTTTTTACGTCTGAAAAAGAGAAGG--AGATCGAACA	287
B_subtilis	241	aaaaatccatattttttaacaggtgaaaagaaaaaagaaaaaattgagca	290
SEQ_177	288	TGATT TGCGAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGA	337
B_subtilis	291	caacgtcagtgcgcttgaatcatatatacaatcacctgcgccttacacag	340
SEQ_177	338	TCGTCGTCTTTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAAAATT	387
B_subtilis	341	tctttgtcctgcttgctccgtatgaaaagcttgatgagcgaaaaaagctg	390
SEQ_177	388	AC-----GAAGCTCGC--CAAAGAGCAAAGCGAAGTCGTCATC	423
B_subtilis	391	acgaaagcgttaaagaagcacgcgttatgatggaggcgaag--gaatta	438
SEQ_177	424	GCCGCCCCG--CTCGCCGAAGCGGAGCTGCGTGCCCTGGGTGCGGCGCCGC	471
B_subtilis	439	aatgcaaaggaaacgac-agactttactgtcaacct--tgcaaaaacag	484

SEQ_177	472	ATCGAGAGCCAAGGGGCGCAAGCAAGCGACGAGGCGATTGATGTCCTG-T	520
		. ... ..   ..   .  . ..... ... ...   . ...	
B_subtilis	485	agcagaaaacaatcggcac--ggaagcggcgggagcatttg--gttctgct	530
SEQ_177	521	TGCGGCGGGCCGGGACGCAGCTTTC--CGCCTTGCGGAATGAAATCGATA	568
		.  ..     ..   .    ... ... ...   ..   .	
B_subtilis	531	tgt---gaacgg--tcatctgtcatcgatttttcaggag-attcaaaa	572
SEQ_177	569	AATTGGCCCTGTTTGCCG--GATCGGGCGGAACCATCGAGGCGGCGGCGG	616
		.. ..   .  ...   ... .. ... ...   .. .. ..	
B_subtilis	573	gctctgcac-gtttattggagatcgtgaagaaattacgc--tggatgatg	619
SEQ_177	617	TTGAGCGGCTTGTCGCCCCGACGCC--GGAAGAAAACGTATTTGTGCTTGT	665
		.. ... ... ... ...   ..     ... ... ... ... ...	
B_subtilis	620	taaaaatgcttggttgctag-aagccttgaacaaaatatttttgagctgat	668
SEQ_177	666	CGAGCAAGTGGCGAAGCGCGACATTCCAGCAGCGT-TGCAGACGTTTTAT	714
		.. ..   .  .. ..   .. ... ...   ..    ... .. ...	
B_subtilis	669	caataaaatcgtcaaccgaaaacgaacag-agagtctgcaaattttttat	717
SEQ_177	715	GATCTGCTTGAAAACAATGAAGAGCCGATCAAAATTTTGGCGTTGCTCGC	764
		.  ... ... ... ...   ... ... ... ... ... ... ...	
B_subtilis	718	gatttgctaaaaacaaaatgaagaaccgatcaaaattatggcgcttatttc	767
SEQ_177	765	CGCCCATTTCGCTTGCTTTCGCAAGTGAAATGGCTTGCCTCCTTAGGCT	814
		... ... ... ... ... ... ... ... ... ... ... ...	
B_subtilis	768	gaatcagttccggctgattctgcagacgaagtacttcgcggaacagggat	817
SEQ_177	815	ACGGACAGGCGCAAATTGCTGCGGCGCTCAAGGTGCACCCGTTCCGCGTC	864
		... ... ... ... ... ... ... ... ... ... ... ...	
B_subtilis	818	acggacaaaaacaaatcgcttctaatctaaaagttcacccatttcgggta	867
SEQ_177	865	AAGCTCGCTCTTGCTCAAGCGGCCCGCTTCGCTGACGGAGAGCT-TGCTG	913
		... ... ... ... ... ... ... ... ... ... ... ...	
B_subtilis	868	aagctggcgatggatcaagcaaggcttttttcagaggaggagctccgttt	917
SEQ_177	914	AGGCGATCAACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGG---	960
		... ... ... ... ... ... ... ... ... ... ... ...	
B_subtilis	918	aattattgaac-agcttgccgtcatggactatgagatgaaaaccgggaaa	966
SEQ_177	961	GCGGTCGATCGCCGGTTGGCCGTTGAGCTGCTTCTGATGC-GCTGGGGCG	1009
		..   .  .. ... ... ... ...   .. ... ... ... ...   ... ...	
B_subtilis	967	aaggacaagcagctcctgctc---gaactgttccttttacagctgttaaa	1013
SEQ_177	1010	CCCGCCCGGCGCAAGCGGGGCGCCACGGCCGGCGG 1044	
		..... ... ... ... ... ... ... ... ... ... ...	
B_subtilis	1014	aagaaatgaaaaaac-gatccccattattga 1044	



#####

# Program: needle  
# Rundate: Wed Aug 23 15:23:37 2006  
# Align\_format: srspair  
# Report\_file: /ebi/extserv/old-work/needle-20060823-15233673591570.output  
#####

#=====

#  
# Aligned\_sequences: 2  
# 1: SEQ\_177  
# 2: B\_licheniformis  
# Matrix: EBLOSUM62  
# Gap\_penalty: 10.0  
# Extend\_penalty: 0.5  
#  
# Length: 1123  
# Identity: 616/1123 (54.9%)  
# Similarity: 616/1123 (54.9%)  
# Gaps: 137/1123 (12.2%)  
# Score: 2964.5  
#  
#  
#=====

SEQ_177	1	ATGCTGG-AACG-----CGTATGGGGAAACAT	26
		.   . . .    .   .   .   .	
B_licheniform	1	atgaaagaggggaaagtgcagatgacggtatttgatggttggaagc-t	49
SEQ_177	27	TGAAAAACGGCGTTTTTC-TCCCCTTTATTATTATACGGCAATGAGCCG	75
		.   .   .   .   .   .   .   .   .   .   .	
B_licheniform	50	tgaaaaaaggcgacattcatcccgtttattgcttggtacgggaaagagacg	99
SEQ_177	76	TTTTTATTAACGGAAACGTATGAGCGATTGGTGAACGCAGCGCTTGGCCC	125
		.. . . . .   .   .   .   .   .   .   .   .   .	
B_licheniform	100	catcttctgcaggagacggttcaaaggatcagacaagccgttggtgatga	149
SEQ_177	126	CGAGGAGCGGGAGTGGAACTTGGCTGTGTACGA-CTGCGAGGAAACGC--	172
		.   .   .   .   .   .   .   .   .   .   .   .	
B_licheniform	150	agagacgaaagactttaacttctcgatatttgatctggaagaagacgcgc	199
SEQ_177	173	-CGATCGAGGCGGCGCTTGAGGAGGCCGAGACGGTGCCGTTTTTCGGCGA	221
		.   .   .   .   .   .   .   .   .   .   .	
B_licheniform	200	tcgatcttgccg----tgaggatgcggaaacctttccgtttatggggga	245
SEQ_177	222	GCGGCG--TGTCATTCTCATCAAGCATCCATATTTTTTTACGTCTGAAA	268
		..         .   .   .   .   .   .   .   .   .   .	
B_licheniform	246	aaggcgtcttgctg-gcgaaaaac--ccggcgtttttaacagctgaaa	292
SEQ_177	269	AAGAGAAGG--AGATCGAACATGAT-TTGGCGAAGCTGGAGGCGTACTT	314
		.         .   .   .   .   .   .   .   .   .	
B_licheniform	293	aaaagaaggataagcttgagcataatctcggtgta-ctggaagcttacat	341
SEQ_177	315	GAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCTTTTTCGCGCCGTACGAGA	364
		. .   .   .   .   .   .   .   .   .   .   .   .	
B_licheniform	342	tacgcagccggcaccttattccgtgtttgttttgcttgcccttatgaaa	391
SEQ_177	365	AGCTTGATGAGCGAAAAAAATTACGAAGCTCGCCAAAGAGCA-----	407
		.     .   .     .   .   .     .   .   .	
B_licheniform	392	agctcgatgaacggaaaaagctgaccaagctcctgaaaaagcatgcgcac	441
SEQ_177	408	-----AAGCGAAGTCGTCATCGCCGCC-----CCGCTCGCCGAAGC	443
		.   .   .   .   .   .   .   .   .   .   .	
B_licheniform	442	atggtggaagcgaag--gaattaaccgccaaagaaacggctgactttatc	489

SEQ_177	444	GGAGCTGCGTGCCTGGGTGCGGCGCCGCATCGAGAGCCAAGGGGCGCAAG	493
B_licheniform	490	-----gcaggcct-----cgcggaagtcggaaggcaaacaaatcgaa	525
SEQ_177	494	C---AAGCGAC-GAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGACGCA	539
B_licheniform	526	cgggaagcggcggaggagct---tgtcctgttatgtcatgcaag-----	566
SEQ_177	540	GCTTTCCGCCTTGCGGAATGAAATCGATAAATTGGCCCTG----TTTGCC	585
B_licheniform	567	tctgtcagccattgccagga---ggttaaaaagctcagtacatatacc	612
SEQ_177	586	GGATCGGGCGGAACCATCGAGGCGGCGGCGGTTGAGCGGCTTGTCGCCCG	635
B_licheniform	613	ggtgaccgcggagagatcacatagaggatgtcagaaagctttagcgag	662
SEQ_177	636	CACGCCGGAAGAAAACGTATTTGTGCTTGTCGAGCAAGTGGCGAAGCGCG	685
B_licheniform	663	agggcttgaacaaaaatattttcgaactgatcaataaggctcgtcaatcgga	712
SEQ_177	686	ACATTCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAAAACAATGAA	735
B_licheniform	713	aacgtacagaagcgctgcagattttctacgatctattaaagcaaatgaa	762
SEQ_177	736	GAGCCGATCAAAATTTTGGCGTTGCTCGCCGCCCATTTCCGCTTGCTTTC	785
B_licheniform	763	gagccgattaataatgatggcgctgattgctaatacagttcaggctgctgat	812
SEQ_177	786	GCAAGTGAAATGGCTTGCTCCTTAGGCTACGGACAGGCGCAAATTGCTG	835
B_licheniform	813	gcagaccaaatatttttctgaccagggatacggacaaaagcaaategcct	862
SEQ_177	836	CGGCGCTCAAGGTGCACCCGTTCCGCGTCAAGCTCGCTCTTGCTCAAGCG	885
B_licheniform	863	caaaccttaaagtgcacccgttcagggtgaaagctggcgatcgagcaggcg	912
SEQ_177	886	GCCCCGTTTCGCTGA-CGGAGAGCTTGCTGAGGCG-ATCAACGAGCTCGCT	933
B_licheniform	913	aggcttttttcagagcag-gagctt---aggaacattatcgagc-agct	956
SEQ_177	934	GACGCC-----GATTACGAAGTGAA---AAGCGGGGCGGTCGATCGCCG	974
B_licheniform	957	--cgccgtgatggattatgaaatgaagacaggcaaaaaagacaa--gcag	1002
SEQ_177	975	GTTGGCCG--TTGAGCTGCTTCTGATG-CGCTGGGGCGCCC GCCCGGCGC	1021
B_licheniform	1003	ct---cctgcttgaactgtttttgctgaagctgctgcagcctcatgaaaa	1049
SEQ_177	1022	AAGCGGGGCGCCACGGCCGGCGG	1044
B_licheniform	1050	aaac-ggcctcctttaa	1065

#####

# Program: needle  
# Rundate: Wed Aug 23 15:29:49 2006  
# Align\_format: srspair  
# Report\_file: /ebi/extserv/old-work/needle-20060823-15294971407139.output  
#####

#=====

#  
# Aligned\_sequences: 2  
# 1: SEQ\_177  
# 2: B\_halodurans  
# Matrix: EBLOSUM62  
# Gap\_penalty: 10.0  
# Extend\_penalty: 0.5  
#  
# Length: 1096  
# Identity: 571/1096 (52.1%)  
# Similarity: 571/1096 (52.1%)  
# Gaps: 119/1096 (10.9%)  
# Score: 2648.0  
#  
#  
#=====

SEQ_177	1	ATG--CTGGAACGCGTATGGGGAAACATTGAAAAACGG--CGTTTTTCTC	46
		.....   ... ... ... ... ... ... ...	
B_halodurans	1	atgaactatttaaaat-taaagcaagatgtccaagcgggacgagtggccc	49
SEQ_177	47	CCCTTTATTTATTATACGGCAATGAGCCGTTTTTTATT-AACGGAAACGTA	95
		.. ... ... ... ... ... ... ... ... ... ... ...	
B_halodurans	50	ctgtatatatttatgtatgggaccgagttgtttttaatggaagacctcata	99
SEQ_177	96	-TGAGCGATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAAC	144
		. .. ... ... ... ... ... ... ... ... ... ...	
B_halodurans	100	caggacattt--tgtccgtaacg-ttatac----ggatgaggaaagggat	141
SEQ_177	145	TTGGCTGTGTACGACTGC-----GAGGAAACGCCGATCGAGGCGGCGC	187
		. ... ... ... ... ... ... ... ... ... ... ...	
B_halodurans	142	atgaatgt-ttcattcttatcccttactgatgttccgattgaggcggcgc	190
SEQ_177	188	TTGAGGAGGCCGAGACGGTGCCGTTTTTTCGGCGAGCGGCGTGTCAATCTC	237
		... ... ... ... ... ... ... ... ... ... ... ...	
B_halodurans	191	tcgaagaagcagaaacggttccttttttggctcgaagcgggtcgtgatc	240
SEQ_177	238	ATCAA---GCATCCATATTTTTTTTACGTCTGAAAAAGAGAAGGAGATCG	283
		. ... ... ... ... ... ... ... ... ... ... ...	
B_halodurans	241	ttaaaagatgctgccctattt-----acaagccaaaagcttgatgttg	283
SEQ_177	284	AACATGATTTGGCGAAGCTGGAGGCGTAC---TTGAA---GGCGCCGTCG	327
		... ... ... ... ... ... ... ... ... ... ... ...	
B_halodurans	284	agcacgatgtgaaacgattggagcaatacatattgaaccagttccagag	333
SEQ_177	328	CCGTTTTTCGATCGTCTCTTTTTTCGCGCCGTACGAGAAGCTTGATGAGCG	377
		. ... ... ... ... ... ... ... ... ... ... ...	
B_halodurans	334	acggttttgcgtgatc-----atggccccttatgaaaagctcgatgaacg	377
SEQ_177	378	AAAAAAAATTACGAAGCTCGCCAAAGAGCAAAGCGAAG-TCGTCATCGCC	426
		... ... ... ... ... ... ... ... ... ...	
B_halodurans	378	aaaaaaaatcacgaagcttatcaaa----aaagagtcgcttggttcttgag	423
SEQ_177	427	GCC---CCGCTCGCCGAAGCGGAGCTGCGTGCCTGGGTG-CGGCGCCGCA	472
		... ... ... ... ... ... ... ... ... ... ...	
B_halodurans	424	gcaaagcctttggacgaaggagaggcaaaagcatggctatcctcactggc	473

SEQ_177	473	TCGAGAGC--CAAGGGGCG-----CAAGCAAGCGA-CGAGGCGATTGATG	514
		.. .      . . . .  . . . . .  . . . .  .	
B_halodurans	474	aagcgagcttcaggtggagatggacgagaaagctatcgagacgt-----	517
SEQ_177	515	TCCTGTTGCGGCGGGCCGGGACGCAGCTT-TCCGCCTTGGCGAATGAAAT	563
		. . . . .  . . . .  . . . .  . . . .  .	
B_halodurans	518	---tggtt-agggatgacgggtcttcgcttgacccaattagcatctgaaat	563
SEQ_177	564	CGATAAATTGGCCCTGTTTGCCGGATCGGGCGGAACCATCGAGGCGGCGG	613
		..     . . . . .  . . . .  . . . .  . . . .  .	
B_halodurans	564	gaataaattagcgttgtagtaggggaaggaggcatcatccgatcagagg	613
SEQ_177	614	CGGTTGAGCGGCTTGTCGCCCGCACGCCGAAGAAAACGTATTTGTGCTT	663
		.. . . . .  . . . .  . . . .  . . . .  . . . .  .	
B_halodurans	614	acgtaaccttgctcgttgctaaaacgctcgatcaaacatatttgatctg	663
SEQ_177	664	GTCGAGCAAGTGGCGAAGCGCGACATTC-----CAGC-AGCGTTGCA	704
		.. .  . .  . .  .  .  .  .  .  .  .  .	
B_halodurans	664	attg---attttgc-----catcaatcagaggactcatcaagcgct-ct	703
SEQ_177	705	GACGTTT-TATGATCTGCTTGAAAACAATGAAGAGCCGATCAAAATTTTG	753
		.. .  .  .  .  .  .  .  .  .  .  .  .  .  .	
B_halodurans	704	ctctttaccatgagctcctgaaacaaaagaggagccattgaagctgttg	753
SEQ_177	754	GCGTTGCTCGC-CGCCCATTTCCGCTTGCTTTCGCAAGTGAAATGGCTTG	802
		.  .  .  .  .  .  .  .  .  .  .  .  .  .	
B_halodurans	754	gccttattaacacggcagttt-cgcatcatgtaccaagtcaaagagcttg	802
SEQ_177	803	CCTCCTTAGGCTACGGACAGGCGCAAATTGCTGCGGCGCTCAAGGTGCAC	852
		.....    .  .  .  .  .  .  .  .  .  .  .  .  .	
B_halodurans	803	gacgaagaggatacaccccgaaatcagatggcgaagccgttaaaaattcat	852
SEQ_177	853	CCGTTCCGCGTCAAGCTCGCTCTTGCTCAAGCGGCCCGCTTCGCTG----	898
		.  .  .  .  .  .  .  .  .  .  .  .  .  .	
B_halodurans	853	ccctatgttgccaaacttgcgggaaaaaaagcagccagcatgtcagacca	902
SEQ_177	899	ACGGAGAGCTTGCTGAGGCGATCAACGAGCTCGCTGACGCCGATTACGAA	948
		.  .  .  .  .  .  .  .  .  .  .  .  .  .	
B_halodurans	903	actgttatattccctaatacg---aaaaagct-gcggatacagagtttgcg	948
SEQ_177	949	GTGAAAAGCGGGGCGGTCGATCGCCGGTTGGCCGTTGAGCTGCTTCTGAT	998
		.. .  .  .  .  .  .  .  .  .  .  .  .  .  .	
B_halodurans	949	attaaaagtggaaaggttgataaagtgctggcattagaattgtttttt---	995
SEQ_177	999	GCGCTGGGGCGCCCCGCCGCAAGCGGGGCGCCACGGCCGGCGG	1044
		.. .  .  .  .  .  .  .  .  .  .  .  .  .  .	
B_halodurans	996	-----actcacaatgggttctag-ggagagcgtaggttag	1029

#####

# Program: needle  
# Rundate: Wed Aug 23 15:33:21 2006  
# Align\_format: srspair  
# Report\_file: /ebi/extserv/old-work/needle-20060823-15332034285052.output  
#####

#=====

#  
# Aligned\_sequences: 2  
# 1: SEQ\_177  
# 2: B\_clausii  
# Matrix: EBLOSUM62  
# Gap\_penalty: 10.0  
# Extend\_penalty: 0.5  
#  
# Length: 1124  
# Identity: 579/1124 (51.5%)  
# Similarity: 579/1124 (51.5%)  
# Gaps: 181/1124 (16.1%)  
# Score: 2671.5  
#  
#  
#=====

SEQ_177	1	ATGCTGGAACGCGTATGGGGAAACATTGAAAAACG-GCGTTTTCTCC	47
		..  ... ... ... ... ... ... ... ... ... ... ...	
B_clausii	1	atgagcatcattacggaaatgaagcaattgtcagtgagacaatggcacc	50
SEQ_177	48	CCTTTATTTATTATACGGCAATGAGCCGTTTATTAAACGGAAACGTATG	97
		.. ... ... ... ... ... ... ... ... ... ... ...	
B_clausii	51	ggtatactttttgtatgggacaga-acgttatt-taatcgagcaattttt	98
SEQ_177	98	AGCGATTGGTGAACGCAGCGCTTGGCCCCGAGGA-----GCGGGAGTG--	140
		... ... ... ... ... ... ... ... ... ... ... ...	
B_clausii	99	a-caaaaagcaagcgaagcattatttgcaggggaagaaggc-gaaatgaa	146
SEQ_177	141	-GAACTTGGCTGTGTACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTT	189
		... ... ... ... ... ... ... ... ... ... ... ...	
B_clausii	147	tgatattcgct---tacgcttac-aagatacgccgctaggggaagtgggtg	192
SEQ_177	190	GAGGAGGCCGAGACGGTGCCGTTTTCGGCCGAGCGG---CGTGTCATTCT	236
		... ... ... ... ... ... ... ... ... ... ...	
B_clausii	193	gaggaagcggagactgttccgtttttctcaaagcggaaacttgttgtgat	242
SEQ_177	237	CATCAAGCATCCATATTTTTTTTACGT--CTGAAA-AAGAGAAGGAGATCG	283
		... ... ... ... ... ... ... ... ... ... ... ...	
B_clausii	243	c--caagact-tttatttggcaacgagccagaaagtagcgacaaaactgg	289
SEQ_177	284	AACATGATTTGGCGAAGCTGGAGGCGTA-CTTGAAGGCGCCGTCGC-CGT	331
		... ... ... ... ... ... ... ... ... ... ... ...	
B_clausii	290	agcatgacattcccgactggaagcctatctcgac-tcgctgcacaaga	338
SEQ_177	332	TTTCGATCGTCGTCTTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAA	381
		... ... ... ... ... ... ... ... ... ... ... ...	
B_clausii	339	aaccgtgc-ttgtcgttgtcgcgccgtatgaaaaattagatgaacgcaag	387
SEQ_177	382	AAAATTACGAAGCTCGCCAAAGAGCAAAGCGAAGTCGTCATCGCCG---C	428
		... ... ... ... ... ... ... ... ... ... ...	
B_clausii	388	aaaatcaccaaaaaattaaaaaaacaaa-cgag--cgctattgatgtgaa	434
SEQ_177	429	CCCGCTCGCCGAAGCGGAGC---TGCCTGCCTGGGTGCGGCGCCGCATC	474
		.. ... ... ... ... ... ... ... ... ... ... ...	
B_clausii	435	tccatttgatgaaaaggaaacatttgcgtggatggaggcgatagctaaac	484



SEQ_177	475	--GAGAGCCAAGGGGCG--CAAGCAAGCGACGAGGCGATTGATGTCCTGT	520
		.    .      .     ...   .   .     .   ..	
B_clausii	485	aggagggc---gttgcgatcgagcaagacgcgaagcaattgctgtat--a	529
SEQ_177	521	TGCG-GCGGGCCGGGAC--GCAGCT-TTCCGCC-----TTGGCGAA-TGA	560
		.     .     ...    . .   . .    .       .	
B_clausii	530	agcgtacaggccctaacttgatggttggtgcaccgtgaattggagaagtgc	579
SEQ_177	561	A-----ATCGATAAATTGG--CCCTGT--TTGCCGGATCGGGCG--GA	597
		.   .    .    .   .   .   .   .	
B_clausii	580	atgttgatatagcaaagacgggggacccagtcacagcaagcattgtcgacga	629
SEQ_177	598	ACCATCGAGGCGGCGGCGGTTGAGCGGC-----TTGTCGCCCG	635
		.   .   .   .   .   .   .   .   .	
B_clausii	630	ac--tcgttgctgagacagtggaacaaagtgtatttactgttattgacta	677
SEQ_177	636	CACGCCGGAAGAAAACGTATTTGTGCTTGTGCGAGCAAGTGGCGAAGCGCG	685
		.   .    .     .   .   .   .   .   .	
B_clausii	678	cacggcgaaag-----gc-----cgtgctggtgacgcggtccg	710
SEQ_177	686	ACATT-CCAGCAGC-GTTGCAGACGTTTTATGATCTGCTTGAAAACAATG	733
		. .      .            .  .    .	
B_clausii	711	gctttaccaccagctgttg-aggc-----aaaaag	739
SEQ_177	734	AAGAGCCGATCAAAATTTTGGCGTTGCTCGCCGC--CCATTTCCGCTTGC	781
		.   .   .   .   .   .   .   .   .   .	
B_clausii	740	aagagccgctggccatactggcggttg-ttgacgcggcaatttcggcaatt	788
SEQ_177	782	TTTCGCAAGTGAAA--TGGCTTGCCTCCTTAGGCTACGGACAGGCGCAA	828
		.      .    .  .    .   .   .   .   .   .	
B_clausii	789	tttc-caggtgaaaacgaggctag--ccaaaggtacacgcaaaaagag	834
SEQ_177	829	ATTGCTGCGGCGCTCAAGGTGCACCCGTTCCGCGTCAAGCTCGCTCTTGC	878
		.   .   .   .   .   .   .   .   .   .   .   .	
B_clausii	835	atggcatcacagcttaaattgcaccccttatgtagtaaagctcgc-catgc	883
SEQ_177	879	TCAAGCGGCCCCGCTTCGCTGACGGAGAGCTTGC--TGAGGCGATC----	921
		.   .   .   .   .   .   .   .   .   .   .   .	
B_clausii	884	---agcaagtcaaagcgtaac--gaccaagcaattaagacaagctctt	927
SEQ_177	922	AACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGGGC-GGTCGATC	970
		.   .   .   .   .   .   .   .   .   .   .   .   .	
B_clausii	928	atcgtttgcaagaactgactatgccattaaga-cagggcaggccgata	976
SEQ_177	971	GCCGGTTGGCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCCGGCG	1020
		....       .     .   .   .   .   .   .   .   .	
B_clausii	977	aagagttggcgcgagctggttgctgctgcgattg--gcaagcacgtaa	1023
SEQ_177	1021	CAAGCGGGGCGCCACGGCCGGCGG	1044
B_clausii	1024		1023

## **Exhibit 3**

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ\_178 348 aa

Sequence 2: G\_kaustophilus 348 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-05445443.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:7434

Alignment Score 2093

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-05445443.aln]

```
SEQ_178      MLERVWGNIEKRRFSPLYLLLYGNEPFLLTETYERLVNAALGPEEREWNLAVYDCEETPIE 60
G_kaustophilus MLERVWGNIEKRRFSLLYLLLYGNEPFLLTETYERLVNAALGPEEREWNLAVYDCEETPVE 60
*****
```

```
SEQ_178      AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
G_kaustophilus AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
*****
```

```
SEQ_178      EKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
G_kaustophilus EKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
*****
```

```
SEQ_178      LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDI PAALQTFYDL 240
G_kaustophilus LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDI PAALQTFYDL 240
*****
```

```
SEQ_178      LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD 300
G_kaustophilus LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD 300
*****
```

```
SEQ_178      GELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHRGRR 348
G_kaustophilus GELAEAINELADADYEVKSGAVDRRLAVELLMLRWGTRPAQAGRHRGRR 348
*****
```

Sequence format is Pearson

Sequence 2: Bacillus sp NRRL B14911 346 aa

Aligning...

Guide tree file created: [/ebi/extserv/clustalw-

work/interactive/clustalw-20060823-05514556.dnd]

### Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5730

Alignment Score 1092

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-05514556.aln]

```
SEQ_178          MLERVWGNIEKRRFSPLYLLYGNEPFLLTETYERLVNAALGPPEEREWNLA 50  
Bacillus_sp_NRRL_B14911 MVLDVWKQINNKKQFTPIYLLYGTEGFLINETKQLLINNVLAEDESDFNLS 50  
*: ** :*::*:**:*:***. * **:.*; *: .*: :***;
```

```

SEQ_178          VYDCEETPIEAALEEAETVPFFGERRVILIKHPYFFTSEKEK-EIEHDLA 99
Bacillus_sp_NRRL_B14911 TYDLEETPIEAALEDAETFPFMGDKRLIFLHNPSFLTSEKTKGKTEHNLA 100
      ** *****.***.*:*::*::::* *::***** * : **:***

```

```
SEQ_178      KLEAYLKAPSPFSIVVFFAPYEKLDERKKITKLAKQSEVVIAAPLAEAE 149
Bacillus_sp_NRRL_B14911 KLESYLKEPSPYSIIVFAAPYEKLDDRKKITKELKKKASVLEAKKLGEQE 150
***.*.*.* *.*.*.*.* *.*.*.*.* *.:*:.*: * *.** *
```

```

SEQ_178                LRAWVRRRIESQGAQASDEAIDVLLRRAGTQLSALANEIDKLALFAGSGG 199
Bacillus_sp_NRRL_B14911 LKVWIRERAAQNGVQIEEDAVQLMLTLAGTNLFMLTGEIDKLALYADEEK 200
* . * . * . * . * . * . * . * . * . * . * . * . * . * . * .

```

```

SEQ_178                               TIEAAVERLVARTPEENVFVLVEQVAKRDIPAAALQTFYDLLNNEEPIK 249
Bacillus_sp_NRRL_B14911             LIDAEAVDKLVARSLQNIFTLVCKVVHRKIDEALRIYYDLLKQNEEPIK 250
          *.* **..... *:.-* **:..*:..*   **: :****: :*****

```

```
SEQ_178 ILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAAARFA 299  
Bacillus_sp_NRRL_B14911 ILSILTGQFRLIYQVKELSRRGYGQQQTAGYLKVHPFRVKLAAGQAQLFG 300  
***.*..**:* ** * ..*** * .***** *****.** *
```

```

SEQ_178          DGELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHRGR 348
Bacillus_sp_NRRL_B14911 DEELSRIMKLLAEADYEMKTGGMNKEMLIEMFLFRLHDHALHKQTK--- 346
* * *: : *****:**: : : : : *::*:~ : : :

```

Sequence format is Pearson

Sequence 2: B cereus cytotoxis 336 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 46

```
Guide tree      file created:  [/ebi/extserv/clustalw-
work/interactive/clustalw-20060823-06030715.dnd]
```

### Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2      Score:5437

Alignment Score 961

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-06030715.aln]

```

SEQ_178                MLERVWGNIEKRRFSPLYLLYGNEPELLTETYERLVNAALGPEEREWNLAVDCEETPIE 60
B_cereus_cytotoxis    -MSDIHKKIKKKQFAPFYLLYGTEAYFINETIDLITVEALAEEDRDFNIVTYDLEEAYLE 59
                        :. : *:*:*:*:*:***.:.:.** : . ** *::*:..** **: :*

```

```

SEQ_178      AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
B_cereus_cytotoxis DVVEDARTLPFFGERKILLIKSPLFLT SQKEK-LEQNIKILEEYIAEPSPFSIMIFIAPY 118
      .:*.*:*****:;:*** * *;*:*** :*::: ** *: *****:~*:***

```

```

SEQ_178      EKLDERKKITKLAKEQSEVVIAAPLAEAE LRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
B_cereus_cytotoxis  EKLDERKKITKLLKKTAEVVEANAMQVQDVRKWIVKRAEEVHVHVEEA AVSL LLELVGSN 178
***** * . *** * : : * : * * . : : : * : : * : : * :

```

```

SEQ_178          LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAAALQTFYDL 240
B_cereus_cytotoxis VTMLAKEMDKLTLYVGTGGDITTKLVSELVPKSVEQNVFALTEKVVKKDIAGAMKILDGL 238
:: **::*****::*** * : *..**:: : *****.*:*:*.*:**..*:: : .*

```

```

SEQ_178          LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD 300
B_cereus_cytotoxis FTQQEPIKLLALLVSQFRLLHQVKELQQRGYGQNQIASHIGVHPYRVKLAMNQTKLESF 298
: :*****:*****:***** *** * : ***** ***: : ***:*****: *: *:

```

```

SEQ_178          GELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHGRR   348
B_cereus_cytotoxis EELKKVIFELAEADYSMKTGKMDKKLVLEFFLMRLNHM-----   336
      ** . * ***.*** :*:~* :*:~***

```



Sequence format is Pearson

Sequence 2: B anthracis 336 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 47

```
Guide tree      file created:  [/ebi/extserv/clustalw-
work/interactive/clustalw-20060823-14525436.dnd]
```

### Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5427

Alignment Score 958

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-14525436.aln]

B anthracis -MSDIHKKIKKKOFAPLYLLYGTEAFFINETIKLITTEALEEBEDREFNVVTYDLEEAYLE 59

[illegible]

B anthracis DVVEDARTLPFFGERKVLLIKSPLELTSQKEK-LEQNIKILEEYIGEPSPFSSILVFVAPY 118

\* \* \* \* \*

B anthracis EKLDERKKITKLLKKTADIVEANAMQVQDVQKWIVARAEEGHVHIDNAAVSLLELVGSN 178

\* \* \* \* \*

B anthracis VTMLAKEMDKLTLYVGMGGEITPKLVAELVPKSVEQN VFALTEKVVKKDIAGAMQILDGL 238

\* \* \*

B anthracis FTQQEPIKLLALLVSQFRLHGVKELQQRGYGONQIASHIGVHPYRVKLMNQTKFFSF 298

\* \* \* \* \*

B anthracis EELKKVIELAEADYSMKTGKMDKKLVLEFFLMRLNHM----- 336

\* \*    :    \*    \* \* \* \* \* \* \*    :    \*    \*    :    \*    :    \* \* \*

# CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ\_178 348 aa

Sequence 2: B\_cereus 336 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 47

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-14582093.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5422

Alignment Score 953

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-14582093.aln]

```
SEQ_178      MLERVWGNIEKRRFSPLYLLYGNEPFLLTETYERLVNAALGPEEREWNLAVYDCEETPIE 60
B_cereus     -MSDIHKKIKKKQFAPLYLLYGTEAFFINETIKLITTEALEEEDREFNVVTYDLEEAYLE 59
              .. :  :*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*
              :~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*

SEQ_178      AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
B_cereus     DVVEDARTLPFFGERKVLLIKSPLFLTSQKEK-LEQNIKILEEYIGEPSPFSILVFPVAPY 118
              .:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*

SEQ_178      EKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
B_cereus     EKLDERKKITKLLKKTADVVEANAMQVQDVQKWIVARADEVHVHIDHAAVSLLELVGSN 178
              *****~*~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*

SEQ_178      LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAALQTFYDL 240
B_cereus     VTMLAKEMDKLTLYVGMGGDITPKLVAELVPKSVEQNVFALTEKVVKKDIAGAMQILDGL 238
              :~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*

SEQ_178      LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD 300
B_cereus     FTQQEPIKLLALLVSQFRLHQQVKELQQRGYQONQIASHIGVHPYRVKLMNQTKFFSF 298
              :~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*

SEQ_178      GELAEAINELADADYEVKSGAVDRRLAVELLLMRWGARPAQAGRHRGRR 348
B_cereus     EELKKVIMELAEADYSMTKGMDKKLVLEFFLMRLNHM----- 336
              ** :~* ~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*:~*~*~*~*~*~*~*~*
```

# CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ\_178 348 aa

Sequence 2: B\_thuringiensis 336 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 47

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15064397.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5424

Alignment Score 955

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15064397.aln]

SEQ_178	MLERVWGNIEKRRFSPLYLLYGNEPFLLTETTYERLVNAALGPEEREWNLAVYDCEETPIE	60
B_thuringiensis	-MSDIHKKIKKKQFAPLYLLYGTEAFFINETIKLITTEALEEEDREFNVVTYDLEEAYLE	59
	.. : :*****:*****.*:*:.** : ... ** :***:*.*** **:	

SEQ_178	AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY	120
B_thuringiensis	DVVEDARTLPFFGERKVLLIKSPLELTSQKEK-LEQNIKILEEYIGEPSFVSILVVFVAPY	118
	.:*.*:*****:*.*** * :*:***:*** :*::: ** *: *****:***.***	

SEQ_178	EKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ	180
B_thuringiensis	EKLDERKKITKLLKKTADVVEANAMQVQDVQKWIVARADEVHVHIDNAAVSLLELVGSN	178
	***** ** : :*** * .: :*: * :. .: .: *:***. .*::	

SEQ_178	LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAALQTFYDL	240
B_thuringiensis	VTMLAKEMDKLTLYVGMGGEITTKLVAEVLPKSVEQNVFALTEKVVKKDIAGAMQILDGL	238
	:: ***:***:*.*** ** * : * .***::: *:***.*.*:*.***:***.***: * .*	

SEQ_178	LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD	300
B_thuringiensis	FTQQEETPIKLLALLVSQFRLLYQVKELQQRGYQONQIASHIGVHPYRVKLAMNQTKFFSF	298
	: :*****:*****.:***** *** * . ***** **: : ***:*****: *: *	

SEQ_178	GELAEAINELADADYEVKSGAVDRRLAVEALLMRWGARPAQAGRHRGRR	348
B_thuringiensis	EELKKVIIELAEADYSMTGKMDKKLVLEFFLMRLNHM-----	336
	** :.* ***:***.:*: * :*:***:***:*** .	

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ\_178 348 aa

Sequence 2: B\_weihenstephanensis 336 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 46

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15141625.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5407

Alignment Score 945

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15141625.aln]

```
SEQ_178      MLERVWGNIEKRRFSPLYLLYGNEPFLLTETYERLVNAALGPEEREWNLAVYDCEETPIE 60
B_weihenstephanensis -MSDIHKKIKKKQFAPLYVLYGTEAYFINETIKLITTEALEEEDREFNVVTYDLEEAYLE 59
      .. :  :****:****:****.*.:*** : :.. **  :****:*** ** : :*

SEQ_178      AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
B_weihenstephanensis DVVEDAHTLPFFGERKVILIKSPLFLTAQKEK-LEQNIKILEEYIGEPSPFSILVVFVAPY 118
      .:****:*****:***** * *:***:*** :****: ** *: *****:***,***

SEQ_178      EKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
B_weihenstephanensis EKLDERKKITKLLKKTADVIEANAMQVQDVQKWIVSRADDEVHVIDNAAVSLLLELVGSN 178
      ***** ** : :*: * .: :*: *: * :. .: .: *:***. .*:

SEQ_178      LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAAALQTFYDL 240
B_weihenstephanensis VTMLAKEMDKLTLYVGMGGEITPKLVTELVPKSVEQNVFALTEKVVKKDIAGAMQILDGL 238
      : : ***:***:***:***.* ** * . * .**.: : *****.*.*:***.*** : .*

SEQ_178      LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD 300
B_weihenstephanensis FTQQEPIKLLALLVSQFRLHQVKELQQRGYGQNQIASHIGVHPYRVKLMNQTKFFSF 298
      : : *****:*****.:***** *** * . ***** **: : ***:*****: *: *:

SEQ_178      GELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHR 348
B_weihenstephanensis EELKKVIIELAEADYSMTGKMDKKLVLEFFLMRLNHM----- 336
      ** :.* ****:****.:*** :****:***:*** .
```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ\_178 348 aa

Sequence 2: B\_subtilis 347 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 43

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15180145.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5401

Alignment Score 905

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15180145.aln]

```
SEQ_178      MLERVWGNIEKRRFSPLYLLYGNEPFLLTETYERLVNAALGPEEREWNLAVYDCEETPIE 60
B_subtilis   MVFDVWKSLKKGEVHPVYCLYGKETYLLQETVSRIRQTVVDQETKDFNLSVFDLEEDPLD 60
              *:  **  .::*  ..  *:*  ***:*.::**  **  .*:  ::::  *  ::::*:**  **  *::

SEQ_178      AALEEAETVPFFGERRVILIKHPYFFTSEKEKE-IEHDLAKLEAYLKAPSPFSIVVFFAP 119
B_subtilis   QAIADAETFPFMGERRLVIVKNPYFLTGEKKKEKIEHNVSALESYIQSPAPYTVFVLLAP 120
              *:  :***.**:*****:~::~*:***:*.**:**  ***::~  *:~::~*:~::~*:~::~*:~::~*

SEQ_178      YEKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGT 179
B_subtilis   YEKLDERKKLTKALKKHAFMMEAKELNAKETTDFTVNLAKEQKTIGTEAAEHLVLLVNG 180
              *****:~*  *:::  ::  *  *  *  ..  .  :::  .  **  :  *:  ..

SEQ_178      QLSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAAALQTFYD 239
B_subtilis   HLSSTFQEIQKLCTFIGDREEITLDDVKMLVARSLQNI FELINKIVNRKRTE SLQIFYD 240
              :***:~:  :***:~*  *  *.  *  *  :  *****:  *:~*  *  :~::~*:~*  .  .  :~*  ***

SEQ_178      LLENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFA 299
B_subtilis   LLKQNEEPIKIMALISNQFRLILQTKYFAEQGYGQKQIASNLKVHPFRVKLAMDAQARLES 300
              **::~*****:***:~:  :***:~  *.~::~*  *****  ***:  *****:~*  *:~:

SEQ_178      DGELAEAINELADADYEVKSGAVDRRLAVELLLMRWGARPAQAGRHRGRR 348
B_subtilis   EEELRLIIEQLAVMDYEMKTGKKDKQLLLELFLLQLLKRNEKNDPHY-- 347
              :  **  *:~*  ***:~*  *~::~*  :~*~::~  *  :  .  *
```



# CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ\_178 348 aa

Sequence 2: B\_licheniformis 354 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 44

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15232593.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5440

Alignment Score 922

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15232593.aln]

```

SEQ_178          MLER-----VWGNIEKRRFSPLYLLYGNEPFLLTETYERLVNAALGPEEREWNLAVY 52
B_licheniformis MKEGKVQMTVFDVWKSLLKKGDHPVYCLYGKETHLLQETVQIRQAVVDEETKDFNFSIF 60
* *              ** .::* : :* * **:*..** ** :*: :*:. * :::*:::

```

```

SEQ_178          DCEETPIEAALAEAETVPFFGERRVILIKHPYFFTSEKEKE-IEHDLAKLEAYLKAPSPF 111
B_licheniformis DLEEDALDLAVEDAETFPFMGERRLVVAKNPAFLTAEKKKDKLEHNLGVLEAYITQPAPY 120
* ** .:: *:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

```

```

SEQ_178          SIVVFFAPYEKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAID 171
B_licheniformis SVFVLLAPYEKLDERKKLTKLLKKHAHMVEAKELTAKETADFIAGLAKSEGKQIEPEAAE 180
*:.*::*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

```

```

SEQ_178          VLLRRAGTQLSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIP 231
B_licheniformis ELVLLCHASLSAIAQEVKKLSTYTGDGEITIEDVRKLVARGLEQNIFELINKVVNRKRT 240
*: . .:.*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

```

```

SEQ_178          AALQTFYDLENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLA 291
B_licheniformis EALQIFYDLLKQNEEPIKMMALIANQFRLLMQTKYFSDQGYGQKQIASNLKVHPFRVKLA 300
*** ***:***:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

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```

SEQ_178          LAQAARFADGELAEAINELADADYEVKSGAVDRRLAVELLLMRWGARPAQAGRHRGR 348
B_licheniformis IEQARLFSEQELRNIEQLAVMDYEMKTGKKDKQLLLELFLKLLQPHEKNGLL--- 354
: ** *: : ** : *:*:* ***:*: *:*: *:*:*: : *

```

# CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ\_178 348 aa

Sequence 2: B\_halodurans 342 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 41

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15293846.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5263

Alignment Score 856

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15293846.aln]

```

SEQ_178      -MLERVWGNIEKRRFSPLYLLYGNEPFLLTETYERLVNAALGPEEREWNLAVYDCEETPI 59
B_halodurans MNYLKLKQDVQAGRVAPVYFMYGTELFMEDLIQDILSVTLSDEERDMNVSSYSLTDVPI 60
              ::  :::  *.:*.:*.:*.:* *.: :  : :.:*.: *.:*.: *.: *.: *.: *.:
              *.:*.:*.:*.:* *.:*.:*.:*.:* *.:*.:*.:*.:* *.:*.:*.:*.:*

SEQ_178      EAALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAP 119
B_halodurans EAALEEAETVPFFGSKRVVILKDAALFTSQK-LDVEHDVKRLEQYILNPVPETVLLIMAP 119
              *****.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*

SEQ_178      YEKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGT 179
B_halodurans YEKLDERKKITKLIKESLVLEAKPLDEGEAKAWLSSLASELQVEMDEKAIETLLGMTGL 179
              ***** *.:*.:*.:*.:* *.:*.:*.:*.:* *.:*.:*.:*.:* *.:*.:*.:*.:* *.:*.:*.:*.:*

SEQ_178      QLSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAALQTFYD 239
B_halodurans RLTQLASEMNKLALYVGEGGIIRSEDVTLLVAKTLDQNIFDLIDFAINQORTHQALSLEYHE 239
              *: *.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*

SEQ_178      LLENNEEPTIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFA 299
B_halodurans LLKQKEEPLKLLALLTRQFRIMYQVKELGRRGYTPNQMAKPLKIHPYVAKLAGKKAASMS 299
              *.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*

SEQ_178      DGELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHRGRR 348
B_halodurans DQLLYSLIEKAADTEFAIKSGKVDKVLALELFLTMGSRESVG----- 342
              * * . *.: *.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*.:*

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1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840.